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Here we have studied a novel growth related protein called Cdc37. We have found that Cdc37 binds to Raf-1 and the Cyclin D partner protein Cdk4. We have examined the role of Cdc37 in Raf-1 signaling and in estrogen receptor function. We have found that Cdc37 is required for the function of Raf-1 in mammalian cells. In addition, we have found that inhibition of Cdc37 also inhibited estrogen function in the human MCF-7 breast cancer cell line.

Moreover, we have investigated the potential role of cdc37 in breast cancer. Cdc37 protein expression was found in all breast cancer cell lines examined. We have also found that the drug geldanamycin which is an inhibitor of the Cdc37 partner protein HSP90 is a potent growth suppressor of the MCF-7 estrogen dependent breast cancer cell line. In a screen of human breast cancer cell lines, we have identified one cell line that has 3-4 copies of the CDC37 gene and has a high level of expression of the cdc37 protein. These results suggest that drugs that would inhibit Cdc37 function may be effective in inhibiting breast cancer growth and would be expected to have fewer side effects than geldanamycin.

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FOREWORD

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Introduction

Cdc37 was initially discovered as a cell cycle gene in the yeast Saccharomyces cerevisiae(Reed, 1980). Its mammalian counterpart interacts with growth regulating kinases including CDK4, c-src, and Raf-1(Dey et al., 1996; Stepanova et al., 1996; Perdew et al., 1997; Silverstein et al., 1998). It is co-expressed with cyclin D1 during mammary epithelial cell proliferation. Since cyclin D is an important gene often amplified in breast cancer(Buckley et al., 1993), this proposal seeks to understand the function of cdc37 and its possible in breast cancer.

We have found that cdc37 targets HSP90 to Raf-1 and is required for Raf activation(Grammatikakis et al., 1999). It is commonly thought that the role of cdc37 is to target HSP90 to specific protein kinases like Raf-1, CDK4 and c-src(Stepanova et al., 1996; Hunter and Poon, 1997). Our work has shown that most of cdc37 is in a constitutive complex with the chaperone protein HSP90(Grammatikakis et al., 1999). Work in both yeast and Drosophila indicates that cdc37 can regulate cell growth(Cutforth and Rubin, 1994; Gerber et al., 1995). To this end, we have examined breast cancer cell lines for indications of genetic alterations of the cdc37 gene and attempted to inhibit cdc37 function with geldanamycin, antisense oligos, and a dominant negative cdc37. We have found that at least one human breast cancer cell line has an amplification of the cdc37 gene. Moreover, consistent with our original hypothesis, the Stepanova et al (2000) have shown that cdc37 causes breast cancer in transgenic mice(Stepanova et al., 2000).

Body

Amplification of the cdc37 locus in a breast cancer cell line (task 2)

We have screened six different breast cancer cell lines (both estrogen-dependent and estrogen-independent) for amplifications and rearrangements in the cdc37 genetic locus. DNA was isolated from the six cell lines and primary human diploid fibroblast cell line as a control and digested with EcoR1. The resulting DNA was southern blotted and probed with a 32P labeled cdc37 cDNA as a control. From Figure 1 it can be seen that one of the cell lines MDA-MB-468 shows a significant amplification of the largest fragment. Quantitative analysis by phosphorimager reveals that this band is amplified 3.5 fold relative to the same band in normal human fibroblasts. Other than these changes in band intensities, no other changes in the structure of the gene were apparent. The structure of the human cdc37 has not been determine, but the chicken gene contains 8 exons that span 8.5 kb of DNA(Huang et al., 1998). Thus, we cannot determine from these data if the entire coding sequence or only a portion of it has been amplified. However, these data represent the first demonstration of a genetic alteration of the cdc37 locus in a human tumor and suggest that cdc37 does play a role in the etiology of human breast cancer.

Enhanced expression of cdc37 in human breast cancer cell lines (tasks 3 and 4)

Since we had an indication of amplification of the cdc37 gene in at least one breast cancer cell line and we have shown that overexpression of cdc37 can lead to Raf activation, we decided to evaluate the levels of cdc37 protein expression in human breast cancer cells. (originally we were planning to look and RNA expression and will still do this, but protein expression is functionally more important). 100 ug of total cellular protein from each of three breast cancer cell lines and the growing IMR-90 fibroblast control was electrophoresed through SDS-PAGE gels and processed for Western blotting with anti-cdc37 antibody. The results are shown in Figure 2. As we have seen before, a doublet band of cdc37 is detected. We believe that the lower band is results from an alternatively

spliced form of the cdc37 mRNA, but we have not ruled out that it may result from differential phosphorylation. We favor the former since transfection of a cDNA expression vector for cdc37 only shows a single 50Kd form. Nevertheless, from the blot it can be seen that the cell lines with DNA amplification, MDA-MB-468 expresses 3 fold more cdc37 than the two other metastatic cell lines. These data are interesting in that data from murine mammary tissue suggest that cdc37 is only expressed in lactating breast tissue(Stepanova et al., 1996).

Expression of p50Cdc37 in MCF-7 cells (Task 4,5)

To determine if the effects of cdc37 on the MAP kinase pathway extend to breast cancer cells, we examined the role of cdc37 in the response to estrogen in the MCF-7 human breast cancer cell line. First we sought to determine whether p50cdc37 is expressed in these cells. Previously it was reported that during lactation in mice there is a strong of regulation of p50cdc37 in breast tissue in vivo(Stepanova et al., 1996). We have begun to determine whether this phenomenon can be recapitulated in breast cells in culture. To this end, MCF-7 human breast cancer cells were incubated in the presence of estrogen and various times after estrogen addition cell lysates were analyzed for the expression of cdc37 mRNA and protein. Results are shown in Fig. 3. Northern blot analysis indicates that there is constitutive expression of the CDC37 mRNA with a slight increase after estrogen addition. However, analysis of protein expression by Western blotting indicates that there is a several fold increase in p50cdc37 protein expression by 24 hours. Thus there may be post translational regulation of CDC37 expression in these cells. Also from these experiments, it appears that there is no gross structural alteration of the Cdc37 mRNA or protein.

Involvement of cdc37 in Raf-1 activation (tasks 7-10)

A major accomplishment of our work has been the demonstration the cdc37 is required for Raf-1 activation in mammalian cells. This is the first demonstration of a function for cdc37 in mammalian cells. Moreover, we have shown that cdc37 does these in part by recruiting HSP90 to Raf-1. This provides a basis for the understanding of how cdc37 can function as an oncogene. This work has been published(Silverstein et al., 1998; Grammatikakis et al., 1999) and the papers are included in the appendix.

Geldanamycin inhibits the growth of the MCF-7 breast cancer cell line (Task 12)

There are currently no available small molecule inhibits cdc37. However, the drug geldanamycin is a specific inhibitor of the cdc37 binding protein HSP90(Stebbins et al., 1997). In so far as the role of cdc37 is to target HSP90 to protein kinases such as CDK4 and Raf-1, then it would be expected that geldanamycin would inhibit the function of the cdc37/HSP90 complex. Geldanamycin has previously been found to have anti-tumor as well as anti-fungal properties(DeBoer et al., 1970; Whitesell et al., 1992; Scheibel and Buchner, 1998). Thus as a first stop toward validating the cdc37/HSP90 complex as a potential target for anti-tumor therapy, we examined the effect of geldanamycin on the growth of the estrogen dependent MCF-7 cell line. As can be seen from the growth curve, in figure 4, 2 ug/ml of geldanamycin which is the dose effective in inhibiting Raf-1 activation completely inhibited the growth of the MCF-7 cell line.

Use of antisense oligos to inhibit cdc37 expression (task 11)

Geldanamycin inhibits HSP90 which effects many cellular processes beyond those of cdc37. In addition, Geldanamycin exhibits significant liver toxicity in vivo which limits its use as a therapeutic agent. In principal, agents that would inhibit cdc37 function should have similar growth inhibitory properties, but be less detrimental to other cellular functions. Thus, cdc37 inhibitors would likely be less toxic and have fewer side effects than cdc37 inhibitors. Thus, to validate this in culture, we have sought to inhibit cdc37 function with antisense oligos and with a dominant negative version of the protein. Two different phosphorothioate antisense oligos were synthesized that spanned the initiator ATG of the human cdc37 mRNA. As controls, sense counterparts of these oligonucleotides were synthesized as well. Each of these oligos, was introduced into MCF-7 cells using Lipofectin according to the manufacturers recommendations at 200 ng/ml. After 24 hours of culture, the cells were harvested and processed for cdc37 expression by western blotting. As can be seen from figure 5, the antisense oligos failed to reduce the level of expression of cdc37 protein relative to the sense controls. At this time, we are not sure if the antisense oligos failed to inhibit the translation of cdc37 or whether they inhibited translation, but that the preexisting cdc37 protein is so stable that very little was degraded over the course of this experiment. Based on other experiments, we think the later is the case. Pulse chase experiments will be done to determine this more precisely. However, if cdc37 is a relatively stable protein, then the antisense oligo approach is likely not to be an effective method for inhibiting cdc37 expression.

Overexpression of wildtype and dominant negative cdc37 in MCF-7 cells (tasks 6,13, 14)

To examine the effects of cdc37 on breast cancer cell growth, we have expressed both the wildtype and dominant negative cdc37 in the MCF-7 breast cell line and determined the effects of this on the cell cycle of these cells. We have found that HSP90 interacts with the C-terminal domain of cdc37 and that in the case of Raf-1, expression of a C-terminally truncated form of cdc37 (p36) inhibits HSP90 accumulation onto Raf-1 and Raf-1 activation(Grammatikakis et al., 1999). Thus, this form of cdc37 is a dominant negative at least with regard to Raf-1 activation and most likely for other cdc37 regulated kinases. Thus, wildtype and p36cdc37 were co-transfected into MCF-7 cells with a green florescent protein expression plasmid as a marker gene for transfected cells. After 48 hours, the cells were harvested, stained with propidium iodide and GFP+ cells were analyzed by FACS for cell cycle distribution based on DNA content. The results are shown in Table 1. In this experiment, neither the wildtype or dominant negative cdc37 had a significant effect on the MCF-7 cells. As a positive control, a plasmid that drives the expression of the CDK4 inhibitor p16 was transfected into these cells, and this plasmid was found to decrease the proportion of cell in S-phase and increase the percentage of cell in G1. Thus, we could have detected growth inhibition in this experiment.

There are several possible explanations as to why this experiment failed to show an effect. With regard to the wildtype cdc37, it may be the case that these cells are already growing at such a robust rate that it may be hard to induce them to grow any faster. In the future, we will examine the effect of cdc37 overexpression in non-transformed breast cell lines which may grow at a slower pace to begin with. Another distinct possibility is that that expression from the transfected plasmids is weak in this cell line. However, the data in Table 1 are the results with cdc37 expressed from the strong elongation factor-1 promoter. A similar experiment with cdc37 driven from the SV40 promoter also showed no effect. Clearly we were able to get expression of GFP and p16 in these experiments, but the level of dominant negative cdc37 may not have been high enough to exert an effect since this is a relatively abundant protein. An alternate possibility is that the MCF-7 cell line is not sensitive to inhibitors of cdc37 despite the fact that it is sensitive to geldanamycin. We will test other breast cancer cell lines to determine whether a subset of them are sensitive to the

dominant negative cdc37. It will be especially interesting to test the MDA-MB-468 which has the amplified cdc37 gene.

The effect of CDC37 on estrogen receptor responses. (task 15)

Estrogen plays a key role in the regulation of breast cancer cell growth. The CDC37 partner Hsp90 has long been implicated in steroid receptor responses(Picard et al., 1990; Pratt, 1993). Recently, CDC37 has also been implicated in response of some steroid receptors(Fliss et al., 1997). In addition, there is evidence that estrogen activates the Raf-1/MAP kinase pathway in these cells(Migliaccio et al., 1996). Therefore, we sought to examine the effects of CDC37 on estrogen receptor activity.

For this purpose, we examined the response of the ERE-luciferase reporter gene in the MCF-7 human breast cancer cell line. The results are shown in Fig. 6. In this cell line in the absence of estrogen, p50cdc37 has little or no effect on the expression of reporter gene. In the presence of estrogen, cotransfection of the p50cdc37 gives a slight enhancement of expression of the reporter gene. In these cells, as expected, estrogen results in a significant 40 fold increase in the expression of reporter gene by itself. Interestingly, cotransfection of the dominant negative p50cdc37ΔC in this cell line, has a dramatic effect on the response to estrogen. Though p50cdc37ΔC had little effect by itself, it was able to decrease the response to estradiol by approximately tenfold. This experiment suggests that CDC37 is required for estrogen receptor response in breast cancer cell line. One caveat to this experiment is that we have failed to see p50cdc37ΔC inhibition of the estrogen response when the estrogen receptor is co-transfected with p50cdc37ΔC. This may indicate a stoichiometric relationship between cdc37 and the estrogen receptor.

To examine the effects of p50cdc37 on estrogen regulation of MAP kinase in MCF-7 cells, we have used a reporter gene assay that is sensitive and specific for the MAP kinase pathway. This assay uses the C-terminal domain of Elk-1 fused to a GAL4 DNA binding domain. Elk 1 binds to and is phosphorylated by MAP kinase. Upon phosphorylation, this fusion gene then transactivates a GAL4 UAS containing reporter gene(Marais et al., 1993). When the reporter gene and GAL4 Elk fusion are cotransfected into MCF-7 cells, robust activation of reporter gene is given by the addition of estradiol. (fig. 6B) This confirms the MAP kinase pathway is activated by estradiol. Cotransfection in addition with wild type p50cdc37 slightly increases the stimulation, although cotransfection of p50cdc37 in the absence of estradiol has little effect. Strikingly, cotransfection of the dominant negative p50cdc37ΔC almost entirely abolished activation of the MAP kinase specific reporter gene. This result indicates that estrogen dependent activation of MAP kinase in human MCF-7 cells requires Cdc37.

Activation of STAT3 in breast cancer cell lines (supplemental task)

It has recently become clear that STAT3 is an oncogene and is constitutively activated in some breast cancers(Bromberg et al., 1998; Turkson et al., 1998; Bromberg et al., 1999). This activation is subsequent to c-src activation which is another cdc37 target kinase. Thus, we have examined several breast cancer cell lines for activation of STAT3 by DNA bandshift analysis. From figure 7, it can be seen that 3 of the cell lines do have constitutively active STAT3. Interestingly, MDA-MB-468, which has amplified and overexpressed cdc37, shows the highest degree of STAT3 activation. In the future, we will determine whether dominant negative cdc37 can inhibit this activation of STAT3.

Gene Array profiling (supplemental task, modification of task 1)

The genome project has led to the development of new technologies for the analysis of gene expression since the submission of the original proposal. Since it has now been shown that cdc37 overexpression causes breast cancer in mice and we have found amplification and overexpression of cdc37 in a human breast cancer cell line, we thought it would be informative to perform gene array expression profiling on this cell line relative to other breast cancer cell lines MB-MDA-231 and ZR-75 as well as to primary human breast epithelial cells (75n) and a p53 immortalized derivative of these cells(MB1)(Delmolino et al., 1993; Gao et al., 1996). To initiate this analysis, we expression profiled these cell lines against a gene array of approximately 5000 known human genes (Research Genetics, GeneFilters GF211). (Additional funds to do this analysis were kindly provided by the New England Medical Center Breast Cancer Center). 33P-labeled cDNA probes were generated against RNA isolated from these cell lines and hybridized to the gene array filters as per the manufacturers protocols (http://www.researchgenetics.com/ products/GF200 protocol.php3). After the filters were washed, they were quantitatively imaged on a Molecular Dynamics phosphorimager and then quantitative data was determined for each gene on the filter with the Research Genetics pathways software. The relative intensity of each spot was compared to the 76n normal human breast epithelial primary cells(Delmolino et al., 1993). Genes that showed two fold or greater changes either positively (red) or negatively (green) were further analyzed for expression patterns by cluster analysis (Eisen et al., 1998). The overall cluster pattern is displayed graphically in figure 6. The log ratios of expression for all the genes analyzed are given in the appendix electronic spreadsheet available an as http://www.cochranlab.org/cluster/breastcells.htm. With the exception of MDA-MB-231, the gross patterns of expression are similar for all cell lines examined probably reflecting their common mammary origins. (It is unclear why MDA-MB-231 has a different pattern). Interestingly, there is a clear cluster of genes which are specifically expressed primarily in the MB-MDA-468 cells that have amplified cdc37. A closeup of this cluster region with the identified genes is also shown in Figure 8. While it is clear that these genes do not have obviously similar functions, there are several genes are interest including signaling proteins and transcription factors. One of the upregulated genes is SMAD1 of the TGF-beta signaling pathway. Growth inhibition of breast cancer cells is correlated with estrogen independent growth. It would be interesting to determine if these cells have altered sensitivity to TGF-beta. Since the STAT transcription factors are activated in this cell line, we would expect that some of the upregulated genes would be regulated by STATs. Consistent with this is the finding that the interferon-gamma regulated gene IP-30 is in this cluster. While these data a promising in terms of pointing to clues for cdc37 function, they are also just a beginning of the analysis. It remains to be seen whether cdc37 overexpression is causative for the induction of these genes. For this, cluster analysis will need to be performed on cells that overexpress cdc37. Moreover, cdc37 may be contributing to the expression of many genes in the non-overexpressed breast cell lines as detectable amounts of cdc37 expression in all breast cell lines that we have examined. For

this analysis, effective inhibitors of cdc37 function need to be developed.

- HSP90 associates with cdc37 and is targeted to Raf-1 by it (Silverstein et al., 1998; Grammatikakis et al., 1999)
- Cdc37 can activate Raf-1 as well as Ras in co-transfection experiments (Grammatikakis et al., 1999)
- A cdc37 mutant that fails to bind to HSP90 functions as a dominant negative(Grammatikakis et al., 1999).
- Dominant negative cdc37 inhibits estrogen receptor function in MCF-7 cells.
- The HSP90 inhibitor geldanamycin inhibits the growth of the MCF-7 cell line.
- The MDA-MB-468 breast cancer cell line has an amplified cdc37 gene and overexpresses the protein.

Reportable Outcomes

- 1. Grammatikakis, N., Lin, J.-H., Grammatikakis, A., Tsichlis, P. N. and Cochran, B. H. (1999). p50^{cdc37} acting in concert with Hsp90 is required for Raf-1 function. Mol. Cell Biol. *19*, 1661-1672.
- 2. Silverstein, A. M., Grammatikakis, N., Cochran, B. H., Chinkers, M. and Pratt, W. B. (1998). p50(cdc37) binds directly to the catalytic domain of Raf as well as to a site on hsp90 that is topologically adjacent to the tetratricopeptide repeat binding site. J Biol Chem 273, 20090-5.
- 3. Database of gene expression in various breast cell lines. Available in the appendix and online at http://www.cochranlab.org/cluster/breastcells.htm.

Conclusions

Our finding that cdc37 is required for Raf-1 activation is the first characterization of a function for cdc37 in mammalian cells. Surprisingly we found that cdc37 could activate Raf-1 as well as the Ras oncogene when co-expressed in insect cells. Moreover, our data indicate that cdc37 functions to recruit HSP90 to Raf-1. These data are consistent with the general hypothesis for cdc37 function that it serves a chaperone for specific protein kinases involved in signaling processes (Hunter and Poon, 1997). These data on there own indicate that cdc37 is a critical protein for growth factor signaling and suggest that it could be a good target for intervention in tumor cell growth. This data is further bolstered by the recent findings that overexpression of cdc37 in mice can lead to breast cancer(Stepanova et al., 2000).

Our finding that the cdc37 genetic locus is amplified in at least one human breast cancer cell line provides the first direct connection between cdc37 and human cancer. Our finding that the HSP90 inhibitor geldanamycin inhibits the growth of the MCF-7 cell line indicates that the cdc37/HSP90 complex is likely to be an effective target for therapy of some breast tumors. The toxicity of geldanamycin limits its clinical use (Supko et al., 1995), but other HSP90 inhibitors or cdc37 inhibitors may prove to less toxic.

As yet our attempts to inhibit breast cancer cell growth with antisense and dominant negative cdc37 have been unsuccessful. This is likely due to technical problems having to do with the stability of the cdc37 protein and the expression of the dominant negative cdc37. Alternatively, we will try to inhibit the growth of the breast cancer cell lines by introducing an anti-cdc37 antibody into the cells. We have now done this successfully in fibroblasts. Further reason to believe that inhibition of cdc37 will inhibit MCF-7 growth is our observation the dominant negative cdc37 will inhibit activation of an estrogen responsive reporter gene in these cells and MCF-7 cells require estrogen for growth. Ultimately, specific small molecule inhibitors of HSP90 need to be developed as has been done for HSP90. Such molecules could be useful both experimentally and clinically.

The recent findings that STAT3 is an oncogene and is activated in some breast cancers is an important new avenue for breast cancer research and cdc37 could likely play a role here(Watson and Miller, 1995; Garcia et al., 1997). STAT3 is believed to be activated by src in breast cancer cells(Garcia et al., 1997). Cdc37 interacts with Src and affects its activity(Dey et al., 1996; Perdew et al., 1997). We have found that STAT3 is constitutively activated by src in several metastatic breast cancer cell lines and that the cell line with amplified cdc37 has the greatest amount of STAT3 activation. Consistent with the finding of STAT3 activation, we have performed initial gene expression profiling of several breast cell lines including the MDA-MB-468 cell line that has amplified cdc37 and activated STAT3. While more cell lines need to be profiled in this way, our initial analysis indicates a cluster of co-regulated genes in the MDA-MB-468 cell line. This cluster of genes will provide new avenues of investigation for cdc37 function and could eventually have diagnostic value if found to be correlated with prognosis or therapeutic outcome.

Our findings have opened the door to the investigation of cdc37 as a new target for breast cancer therapy. The recent finding that cdc37 causes breast cancer in mice by the Harper lab reinforces our findings. We are only at the beginning of the quest to understand this gene and unfortunately very few labs are working on this clearly important gene. We hope that our work will stimulate further interest in cdc37 gene and its role in breast cancer.

References

Bromberg, J. F., Horvath, C. M., Besser, D., Lathem, W. W. and Darnell, J. E., Jr. (1998). Stat3 activation is required for cellular transformation by v-src. Mol Cell Biol 18, 2553-8.

Bromberg, J. F., Wrzeszczynska, M. H., Devgan, G., Zhao, Y., Pestell, R. G., Albanese, C. and Darnell, J. E., Jr. (1999). Stat3 as an oncogene. Cell 98, 295-303.

Buckley, M. F., Sweeney, K. J., Hamilton, J. A., Sini, R. L., Manning, D. L., Nicholson, R. I., deFazio, A., Watts, C. K., Musgrove, E. A. and Sutherland, R. L. (1993). Expression and amplification of cyclin genes in human breast cancer. Oncogene 8, 2127-33.

Cutforth, T. and Rubin, G. M. (1994). Mutations in Hsp83 and cdc37 impair signaling by the sevenless receptor tyrosine kinase in Drosophila. Cell 77, 1027-36.

DeBoer, C., Meulman, P. A., Wnuk, R. J. and Peterson, D. H. (1970). Geldanamycin, a new antibiotic. J Antibiot (Tokyo) 23, 442-7.

Delmolino, L., Band, H. and Band, V. (1993). Expression and stability of p53 protein in normal human mammary epithelial cells. Carcinogenesis 14, 827-32.

Dey, B., Lightbody, J. J. and Boschelli, F. (1996). CDC37 is required for p60v-src activity in yeast. Mol Biol Cell 7, 1405-17.

Eisen, M. B., Spellman, P. T., Brown, P. O. and Botstein, D. (1998). Cluster analysis and display of genome-wide expression patterns. Proc Natl Acad Sci U S A 95, 14863-8.

Fliss, A. E., Fang, Y., Boschelli, F. and Caplan, A. J. (1997). Differential In Vivo Regulation of Steroid Hormone Receptor Activation by Cdc37p. Mol Biol Cell 8, 2501-9.

Gao, Q., Hauser, S. H., Liu, X. L., Wazer, D. E., Madoc-Jones, H. and Band, V. (1996). Mutant p53-induced immortalization of primary human mammary epithelial cells. Cancer Res *56*, 3129-33.

Garcia, R., Yu, C. L., Hudnall, A., Catlett, R., Nelson, K. L., Smithgall, T., Fujita, D. J., Ethier, S. P. and Jove, R. (1997). Constitutive activation of Stat3 in fibroblasts transformed by diverse oncoproteins and in breast carcinoma cells. Cell Growth Differ 8, 1267-76.

Gerber, M. R., Farrell, A., Deshaies, R. J., Herskowitz, I. and Morgan, D. O. (1995). Cdc37 is required for association of the protein kinase Cdc28 with G1 and mitotic cyclins. Proc Natl Acad Sci U S A 92, 4651-5.

Grammatikakis, N., Lin, J.-H., Grammatikakis, A., Tsichlis, P. N. and Cochran, B. H. (1999). p50cdc37 acting in concert with Hsp90 is required for Raf-1 function. Mol. Cell Biol. 19, 1661-1672.

Huang, L., Grammatikakis, N. and Toole, B. P. (1998). Organization of the chick CDC37 gene. J Biol Chem *273*, 3598-603.

- Hunter, T. and Poon, R. Y. C. (1997). Cdc37: a protein kinase chaperone? Trends in Cell Biol. 7, 157-161.
- Marais, R., Wynne, J. and Treisman, R. (1993). The SRF accessory protein Elk-1 contains a growth factor-regulated transcriptional activation domain. Cell 73, 381-393.
- Migliaccio, A., Di Domenico, M., Castoria, G., de Falco, A., Bontempo, P., Nola, E. and Auricchio, F. (1996). Tyrosine kinase/p21ras/MAP-kinase pathway activation by estradiol-receptor complex in MCF-7 cells. Embo J 15, 1292-300.
- Perdew, G. H., Wiegand, H., Vanden Heuvel, J. P., Mitchell, C. and Singh, S. S. (1997). A 50 kilodalton protein associated with raf and pp60(v-src) protein kinases is a mammalian homolog of the cell cycle control protein cdc37. Biochemistry 36, 3600-7.
- Picard, D., Khursheed, B., Garabedian, M. J., Fortin, M. G., Lindquist, S. and Yamamoto, K. R. (1990). Reduced levels of hsp90 compromise steroid receptor action in vivo. Nature 348, 166-8.
- Pratt, W. B. (1993). The role of heat-shock proteins in regulating the function, folding and trafficking of the glucocorticoid receptor. J. Biol. Chem. 268, 21455-21458.
- Reed, S. I. (1980). The selection of S. cerevisiae mutants defective in the start event of cell division. Genetics 95, 561-77.
- Scheibel, T. and Buchner, J. (1998). The Hsp90 complex--a super-chaperone machine as a novel drug target. Biochem Pharmacol *56*, 675-82.
- Silverstein, A. M., Grammatikakis, N., Cochran, B. H., Chinkers, M. and Pratt, W. B. (1998). p50(cdc37) binds directly to the catalytic domain of Raf as well as to a site on hsp90 that is topologically adjacent to the tetratricopeptide repeat binding site. J Biol Chem 273, 20090-5.
- Stebbins, C. E., Russo, A. A., Schneider, C., Rosen, N., Hartl, F. U. and Pavletich, N. P. (1997). Crystal structure of an Hsp90-geldanamycin complex: targeting of a protein chaperone by an antitumor agent. Cell 89, 239-50.
- Stepanova, L., Finegold, M., DeMayo, F., Schmidt, E. V. and Harper, J. W. (2000). The oncoprotein kinase chaperone CDC37 functions as an oncogene in mice and collaborates with both c-myc and cyclin D1 in transformation of multiple tissues. Mol Cell Biol 20, 4462-73.
- Stepanova, L., Leng, X., Parker, S. and Harper, J. (1996). Mammalian p50^{Cdc37} is a protein kinase-targeting subunit of Hsp90 that binds and stabilizes Cdk4. Genes & Dev 10, 1491-1502.
- Supko, J. G., Hickman, R. L., Grever, M. R. and Malspeis, L. (1995). Preclinical pharmacologic evaluation of geldanamycin as an antitumor agent. Cancer Chemother Pharmacol 36, 305-15.
- Turkson, J., Bowman, T., Garcia, R., Caldenhoven, E., De Groot, R. P. and Jove, R. (1998). Stat3 activation by Src induces specific gene regulation and is required for cell transformation. Mol Cell Biol *18*, 2545-52.

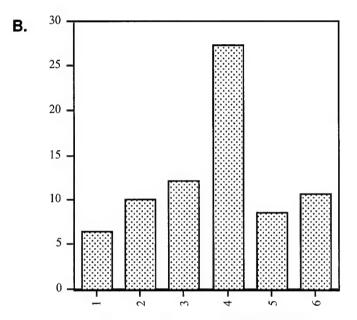
Watson, C. J. and Miller, W. R. (1995). Elevated levels of members of the STAT family of transcription factors in breast carcinoma nuclear extracts. Br J Cancer 71, 840-4.

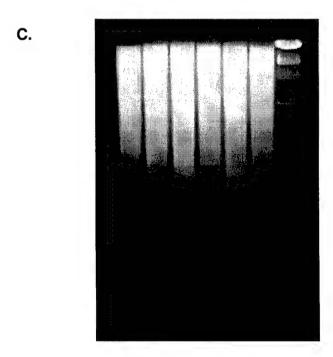
Whitesell, L., Shifrin, S. D., Schwab, G. and Neckers, L. M. (1992). Benzoquinonoid ansamycins possess selective tumoricidal activity unrelated to src kinase inhibition. Cancer Res 52, 1721-8.

Fig 1. Amplification of the cdc37 locus in a breast cancer cell line.

DNA was isolated from the indicated breast cancer cell lines and the human primary diploid fibroblast cell line IMR90 and digested with EcoR1 and separated on a 0.8 % agarose gel and blotted onto Genescreen. A. Full length cdc37 cDNA was labelled with 32p and hybridized to the immobilized DNA on nitrocellulose and exposed to X-ray film. B. Graph showing quantitation of the band on the phosphorimager. C. Ethidium bromide stain of the gel to show equal loading.







MDA-MB-231 MDA-MB-435 — cqc37

Fig. 2. Cdc37 expression in breast cancer cell lines. Extract were prepared from the indicated breast cancer cell lines and electophoresed through SDS-PAGE gels and processed for Western blotting with anti-cdc37 antisera.

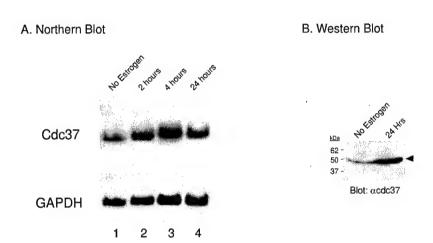


Fig. 3. Expression of CDC37 mRNA and protein in MCF-7 cells.

A. Confluent MCF-7 cells were serum starved overnight in serum-free/phenol-red free DMEM and treated with 10 nM estradiol for an indicated amount of time. Total cell RNA was analyzed by Northern. For Cdc37, a internal coding sequence of cdc37 (SmaI fragments) were used as probes. B. Similar as in A, but cells were directly lysed in SDS-PAGE sample buffer and then processed for Western Blotting using the anti-p50cdc37 antibody.

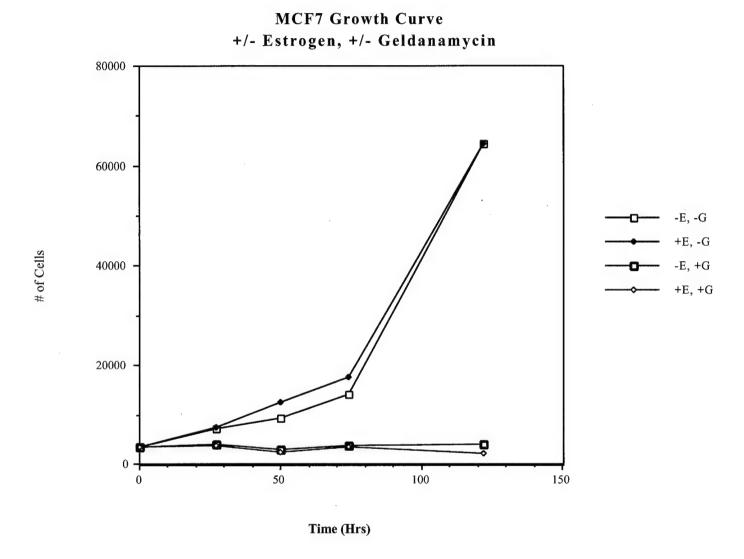


Fig. 4. Inhibition of MCF-7 growth by geldanamycin. Identical parallel cultures of MCF-7 cells in the presence or absence of additional 10 nm estradiol (E) were grown in the presence or absence of 2 ug/ml geldanamycin (G) for the indicated times and cells counted. Note: The basal gowth medium contained estrogen in this experiment.

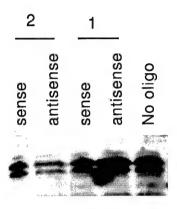
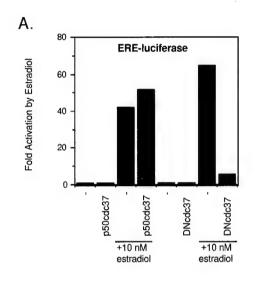


Figure 5. Effect of antisense oligos on cdc37 expression. Phosphorothiate oligos directed toward the ATG codon of human cdc37 were introduced into growing MCF-7 cells at a concentration of 200 nM using lipofectamine. Extracts were prepared 24 hours later and processed for Western blotting with anti-cdc37 antiserum. Complementary sense oligonucleotides were used as conrols for non-specific effects. The sequences of the oligos were as follow: antisense 1: CCACACGCTGTAGTCCACCATCTT, sense 1: AAGATGGTGGACTACAGCGTGTGG, antisense 2: CGTCATTTAAGACATGCAGACTCAT, sense 2: ATGAGTCTGCATGTCTTAAAT-GACG

plasmid	Cell cycle Distribution of GFP positive cells [%] G_0G_1 S G_2M		
cdc37 (p50)	62	33	6
cdc37 ΔC (p36)	61	31	9
p16	69	24	8
pEBG vector	61	35	5

Table 1. Cell cycle analysis by flow cytometry of breast cancer MCF7 cell line transiently overexpressing cdc37 (p50) and cdc37 Δ C (p36) protein forms. Cdk inhibitor, p16, was used as control cell cycle inhibitor.

MCF7 cells were split from a confluent culture 1:5 to equal density and cotransfected on the next day with Fugene 6 (Boehringer) mixed with 14 µg of indicated plasmid DNA and 2 µg of EGFPF (Clontech) used as a marker of transfection for each 60-mm dish. Transfections were performed in duplicates. After 16 hours, the cells were washed with phosphate buffered saline (PBS) and grown for additional 48 hours in fresh Dulbecco's minimum essential medium (DMEM) with 10% fetal bovine serum (FBS). Then, cells were harvested by mild trypsinization followed by 5 minutes incubation in 2 ml DMEM with 10% FBS in room temperature, washed with 5 ml PBS. Pelleted cells were fixed with methanol for 8 minutes on ice, washed with PBS and incubated in 50 μg/ml propidium iodide (PI), prepared afresh from 20 x stock, and 100 μg/ml DNA-free RNase A in 37°C for 15 min. and for additional 30 min on ice. Flow cytometry analysis of cell samples was performed on a Becton Dickinson FACScan and acquired data were analysed using ModFit software for cell cycle profile as represented by PI signal in FL3 channel measuring DNA content. For identification of transfected cells, GFP-positive cells were gated as at least 20 times brighter in FL1 channel than the GFP-negative untransfected cells in the same sample. Percentages of cells in G₀G₁, S and G₂M cell cycle phases in least 10,000 GFP-positive cells within samples transfected with insert-containing vectors were compared to corresponding percentage values of GFP-negative cells within the same sample. The difference was compared to the difference obtained for vector-alone transfected controls and the resulting values are presented in a table above.



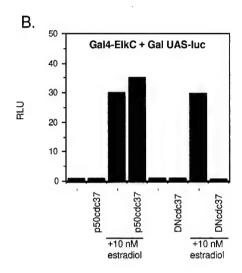


Fig. 6. Inhibition of estogen action in MCF-7 cells by dominant negative Cdc37.

A. MCF-7 cells in phenol-free DMEM were transfected with 50 ng ERE-luciferase and the indicated p50cdc37 expression plasmid per well (24-well plate) using Fugene-6 (Boerhinger-Mannheim). Next day, estrogen was added, and cell were incubated for 24 additional hours until lysis and measurement of luciferase activity. TK-Renillin luciferase activity was used as transfection efficiency control.

B. Similar to A except that the detection system used is the Stratagene Path Detect system for Elk1. This consists of a Gal4 DNA binding domain fused to the Elk-1 C-terminal activation domain and a Gal4 UAS driving a luciferase reporter gene. DNcdc37 is the dominant negative p50cdc37ΔC.

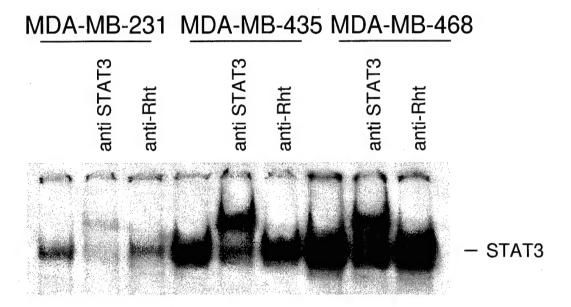


Figure 7. Activaton of STAT3 in breast cancer cell lines. Nuclear extracts were prepared from the indicated breast cancer cell lines and incubated with the 32-P labelled high affinity SIE probe derived from the c-fos gene. To the indicated binding reactions were added antisera to either STAT3 or the unrelated Rht protein as a control for nonspecific interaction. The binding reaction was electorphoresed through 0.5X TBE gels and exposed to X-ray film.

Gene expression cluster analysis of mammary epithelial and breast cancer cell lines. 33P-labeled cDNA probes were generated against RNA isolated from the indicated cell lines and hybridized to the named human gene filters (GF211) as per the manufacturers protocols (http://www.researchgenetics.com/ products/GF200 protocol.php3). After the filters were washed, they were quantitatively imaged on a Molecular Dynamics phosphorimager and then quantitative data was determined for each gene on the filter with the Research Genetics pathways software. The relative intensity of each spot was compared to the 76n normal human breast epithelial primary cells(Delmolino et al., 1993). Genes that showed two fold or greater changes either positively (red) or negatively (green) were further analyzed for expression patterns by cluster analysis using the Stanford cluster software (Eisen et al., 1998). The brightness of the color reflects the relative induction or repression of each gene. The lefthand panel shows the entire profile of The log ratios of expression for all the genes analyzed are given in the appendix and are available as an electronic spreadsheet file online at http://www.cochranlab.org/cluster/breastcells.htm. YY1 is a neomycin resistant subclone of ZR75 and YY3 is an estrogen independent subclone ZR75 that expressed the AND1 gene (Supplied by L. Fieg). MP1 is a p53 immortalized derivative of 76n and 468 and 231 are the estrogen independent breast cancer cell lines MDA-MB-468 and MDA-MB-231 respectively (Supplied by V. Band).

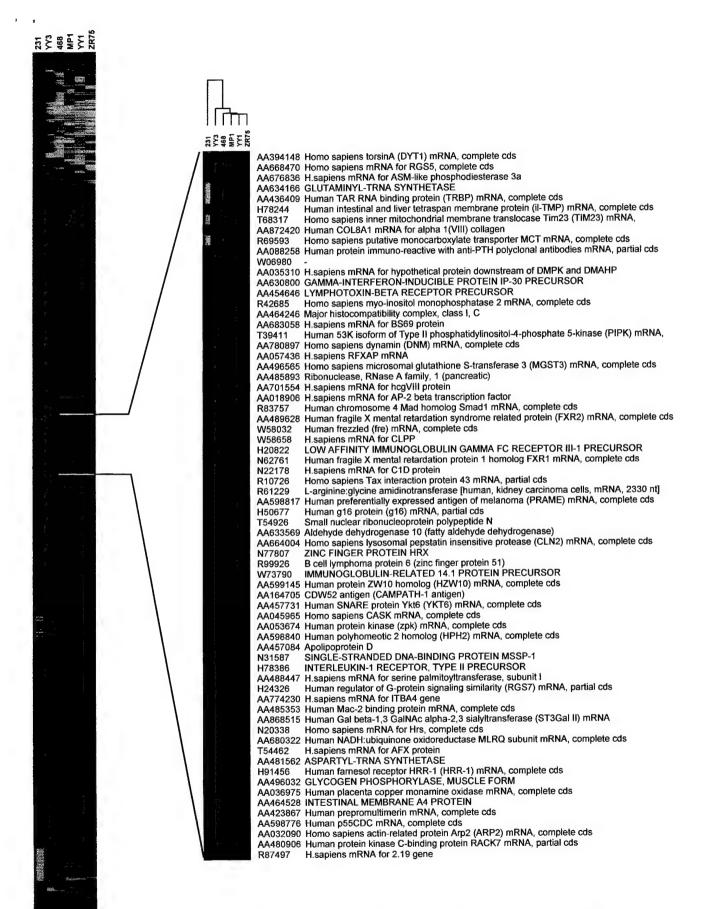


Figure 6. Cluster analysis of gene expression in breast cell lines

p50^{cdc37} Acting in Concert with Hsp90 Is Required for Raf-1 Function†

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Genetic screens in *Drosophila* have identified p50^{cdc37} to be an essential component of the sevenless receptor/mitogen-activated kinase protein (MAPK) signaling pathway, but neither the function nor the target of p50^{cdc37} in this pathway has been defined. In this study, we examined the role of p50^{cdc37} and its Hsp90 chaperone partner in Raf/Mek/MAPK signaling biochemically. We found that coexpression of wild-type p50^{cdc37} with Raf-1 resulted in robust and dose-dependent activation of Raf-1 in Sf9 cells. In addition, p50^{cdc37} greatly potentiated v-Src-mediated Raf-1 activation. Moreover, we found that p50^{cdc37} is the primary determinant of Hsp90 recruitment to Raf-1. Overexpression of a p50^{cdc37} mutant which is unable to recruit Hsp90 into the Raf-1 complex inhibited Raf-1 and MAPK activation by growth factors. Similarly, pretreatment with geldanamycin (GA), an Hsp90-specific inhibitor, prevented both the association of Raf-1 with the p50^{cdc37}-Hsp90 heterodimer and Raf-1 kinase activation by serum. Activation of Raf-1 via baculovirus coexpression with oncogenic Src or Ras in Sf9 cells was also strongly inhibited by dominant negative p50^{cdc37} or by GA. Thus, formation of a ternary Raf-1-p50^{cdc37}-Hsp90 complex is crucial for Raf-1 activity and MAPK pathway signaling. These results provide the first biochemical evidence for the requirement of the p50^{cdc37}-Hsp90 complex in protein kinase regulation and for Raf-1 function in particular.

The mitogen-activated protein kinase (MAPK) phosphorylation cascade, composed of Raf kinase, Mek (MAPK kinase), and Erk (MAPK) itself, relays proliferative and differentiative signals from the plasma membrane to the transcriptional and cell cycle progression machinery (38). Although it is established that Ras-GTP is required to tether Raf-1 to the plasma membrane (reviewed in reference 1), the subsequent events that lead to Raf-1 activation are poorly understood. The major reasons for this are (i) only a small fraction (\sim 3%) of the total Raf-1 cytoplasmic pool needs to become activated for effective signaling (23) and (ii) the entire process of Raf-1 plasma membrane recruitment and activation is rapid and transient (for reviews, see references 37 and 45). Thus, identification of both crucial intermediates and the causative relationships in Raf-1 activation has been difficult. However, it is clear that the N-terminal domain of Raf-1 acts to repress the activity of the C-terminal kinase domain and that its deletion results in constitutive activation of the kinase (25, 68). Phosphorylation of Raf-1 and association with other proteins in response to receptor activation most likely leads to a conformational change in Raf-1 that relieves this repression (37, 45).

Raf-1 fractionated from various cell types exists in large (300- to 500-kDa) multiprotein complexes (78). Known Raf-1-associated proteins include 14-3-3, Hsp90, and pp50, a 50-kDa Hsp90-associated protein (45, 78). 14-3-3 is required for Raf-1 function but probably is not directly involved in the Raf-1 activation process (37, 42, 44). The function of the pp50-Hsp90 complex in Raf-1 activation has yet to be addressed. pp50 had previously been widely found in Hsp90-containing kinase complexes, notably involving v-Src (reviewed in reference 4), and

with both cytoplasmic and membrane localized Raf-1 (66, 78). Hsp90-associated pp50 has recently been identified immunologically and by peptide mapping to be the 50-kDa gene product of the mammalian Cdc37 homologue p50^{cdc37} (51).

Cdc37 was originally identified in yeast as a cell cycle mutant that gives a G₁ cell cycle arrest phenotype (56). Cutforth and Rubin (8) subsequently isolated an allele of Drosophila Cdc37 (Dcdc37) that functioned as a dominant enhancer of the sevenless phenotype in the Drosophila eye. However, these genetic experiments have not identified where and how Dcdc37 functions in the sevenless mitogen-activated protein kinase (MAPK) pathway. Vertebrate Cdc37 was cloned first from chicks (21, 27) and subsequently from mammals (20, 33, 50, 51, 69). The structure of Cdc37 reveals no significant homologies to proteins of known function. The yeast protein is homologous to mammalian and Dcdc37 through only the first 30 amino acids and diverges significantly thereafter. Despite this limited homology, Dcdc37 will complement the yeast gene (8). The cell cycle phenotype of cdc37 appears to be due to a diminished capacity of G_1 cyclins and the cyclin-dependent kinase Cdc28 to associate (19). Subsequent work by ourselves and others has found that mammalian p50^{cdc37} interacts with Cdk4 and accumulates Hsp90 to it (9, 20, 33, 69). Though p50^{cdc37} has been found to interact with diverse kinase families, its interactions are selective in that, for instance, among cyclin-dependent kinases, it interacts with Cdk4 and the closely related Cdk6 but not with Cdk2 (9, 28, 69). Thus, from genetic studies, Cdc37 appears to operate in both the cell cycle and the Ras/Raf/ MAPK pathway in close cooperation with its Hsp90 chaperone

Hsp90 is an abundant and highly conserved protein (54) that is essential in yeast and *Drosophila* (2, 8). Unlike the more general Hsp70 and Hsp60 chaperones, Hsp90 appears to have substrate-specific folding activity (30, 47, 54). It has been best characterized for its essential role in steroid hormone receptor signaling, where it interacts with and modulates receptor func-

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[†] N.G. dedicates this paper to John, George, and Bill.

tion through a dynamic and regulated series of interactions with a defined set of chaperone cofactors (54, 65). Hsp90's conformation and activity have been proposed to be regulated by nucleotide binding, and its associations and activity can be inhibited by geldanamycin (GA) an Hsp90-specific antibiotic which competes for ATP binding to Hsp90 (22, 55). It has been further proposed that p50^{cdc37} may serve to target Hsp90 to a subset of protein kinases and thereby help them achieve an active conformation (28, 53). However, the distantly related yeast Cdc37p by itself has been shown to have chaperone activity in vitro (32).

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The available mammalian association data (63, 66, 78), although not informative about the functional significance of Raf-1 association with Hsp90 and p50cdc37, nevertheless are complemented by genetic evidence from Drosophila. Cutforth and Rubin (8) found that Hsp90 mutations enhance the sevenless phenotype in the Drosophila eye as does Dcdc37 and thus also functions in the MAPK pathway. Subsequently, van der Straten et al. (76) identified Hsp90 alleles that suppress the multiple R7 phenotype caused by the constitutive high-level activation of a membrane-targeted D-Raf kinase domain (Raftor Y9). In fact, the two Hsp90 point mutations recovered in this screen were the strongest dominant suppressors of the multiple R7 photoreceptor cell phenotype caused by the Rasindependent, activated Torso RTK-Raf chimeric protein. Importantly, the mutant Hsp90 proteins identified in these genetic screens exhibited reduced binding to D-Raf-1 and correlated with diminished Raf kinase activity (76). Thus, neither deletion of the N-terminal suppression domain nor membrane anchoring bypasses the requirement of D-Raf-1 for Hsp90 association.

Here, we have addressed directly the biochemical role of p50^{cdc37} and its partner, Hsp90, during Raf-1 activation and signaling to Mek and Erk. We found that p50^{cdc37} and Hsp90 each interact directly with Raf-1 but that p50^{cdc37} is the main determinant of the assembly of heterotrimeric complex. Disruption of the Raf-1-p50^{cdc37}-Hsp90 ternary complex with the Hsp90 inhibitor GA or with a dominant negative p50^{cdc37} inhibits Raf-1 activity. Serum stimulation promotes Raf-1-p50^{cdc37}-Hsp90 complex formation and coexpression of p50^{cdc37} with Raf-1 in insect cells is sufficient to activate Raf-1. Moreover, p50^{cdc37} synergizes with Src for Raf-1 activation. Our data, coupled with the aforementioned genetic studies, indicate that p50^{cdc37} and Hsp90 are critical components of the MAPK cascade and of the Raf-1 activation complex in particular.

MATERIALS AND METHODS

Cell culture and transfections. Cos-1 cells were maintained in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS) and 0.1 µg of penicillin and streptomycin per ml. Freshly plated cells were transfected at 70 to 80% confluence with a total of 7.5 µg of DNAs per 100-mm-diameter dish, using Lipofectamine (Life Technologies) or Targefect (Targetting Systems, San Diego, Calif.). In experiments requiring replicate transfected cultures, cells were split 24 h after the start of transfection into appropriate smaller dishes so that 20 to 24 h later cultures would have achieved confluence. At this point, cells were serum starved for an additional 16 to 18 h. For stimulations, serum (at 20%) or epidermal growth factor (EGF; 100 ng/ml) was directly added for 5 more min before cells were lysed. A 2-mg/ml stock solution of geldanamycin GA in dimethyl sulfoxide (DMSO) or DMSO alone was diluted 1:1,000 in the culture media for the times indicated before cells were either lysed directly or serum stimulated. Solubilized cell extracts were then quantitated for protein content by the Bradford assay and analyzed by direct Western blotting or by protein purification using antibodies or, for overexpressed glutathione S-transferase (GST) fusion proteins, by glutathione (GSH)-Sepharose chromatography, followed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and immunoblotting. Baculovirus infection and culture of Spodoptera frugiperda St9 cells was performed essentially as described by Morrison (43). Unless otherwise indicated, all baculoviruses were infected at comparable levels of multiplicity of infection (MOI).

Antibody reagents. The anti-p50°dc37 antibodies were raised in rabbits against the chick (pNG13 clone [21]) or human GST-p50°dc37 protein. Anti-epitope tag antibodies obtained from Boehringer (antihemagglutinin [anti-HL4] 12CA5 and anti-Mye 9E10) or from Kodak (anti-FLAG M5). Santa Cruz Biotechnology was the supplier for additional antibodies, including ones against Raf-1 (C-12) and GST (Z-5). Monoclonal antibodies against Raf-1 and p50°dc37, used in the experiment described in Fig. 1B, were purchased from Transduction Laborato-ries. Anti-active MAPK polyclonal antibody V6671 was obtained from Promega, and antibodies directed against Hsp90 (SPA-830 and SPA-771) and recombinant human Hsp90 purified from Escherichia coli (SPP-771) were obtained from Stresseen.

Cloning and constructs. For eukaryotic expression, the complete open reading frame for the human p50°ctc37 cDNA was subcloned by PCR into the EcoRI sites of pMT3 and pSG5 vectors and in frame with N-terminal HA and FLAG, respectively, peptide epitopes. Similarly, GST-p50°ct27 constructs were placed by PCR into the BamHI-NotI sites of the pEBG eukaryotic (57) and pGEX2T (Pharmacia) prokaryotic expression vectors. For expression in insect (S. frugi-perda Sf9) cells, the entire open reading frame for the FLAG-p50°ctc37 into protein was subcloned from the pSG5 constructs into the EcoRI/NotI sites of the pFASTBAC1 (Life Technologies) baculovirus vector. Deleted versions of the FLAG-p50°ctc37 fusion protein were produced by using appropriate enzyme disestion of the full-length inserts in pSG5, followed by agarose gel electrophoresis and DNA religation and further subcloned into pFASTBAC1 by the same approach. Cloned inserts were verified by DNA sequencing. Expression plasmids for Raf-1, Ras, and v-Src used in this study have been described previously (14, 35, 46, 63).

In vitro synthesis of radiolabeled p50°cdc37. Different full-length and deletion forms of p50°cdc37 were transcribed and translated in vitro from the pSG5 expression constructs in the presence of 20 μCi of [³⁵S]methionine (EXPRESS protein labeling mix; NEN), using the coupled rabbit reticulocyte lysate and T7 RNA polymerase system (Promega).

Metabolic labeling. Nontransfected or transfected cells 48 to 60 h posttransfection were initially incubated for 2 h in methionine-free medium containing 2% dialyzed fetal serum and then labeled for 4 h with [35S]methionine (NEN) in fresh medium. Cells were then lysed, and equal amounts (counts per minute) of labeled lysate were immunoprecipitated, as described below for nonlabeled ly-

sates, and analyzed by SDS-PAGE and fluorography.

Immunoprecipitation and immunoblotting. Cells were harvested 48 to 60 h after transfection and extracted in Nonidet P-40 lysis buffer (NP-40 LB; 0.5% NP-40, 20 mM HEPES [pH 7.5], 0.1 M NaCl, 2 mM EGTA, 10% glycerol, 50 mM glycerophosphate, 2 mM dithiothreitol [DTT]) containing protease and phosphatase inhibitors (2 mM sodium vanadate, 1 mM NaF, 0.2 mM phenylmethylsulfonyl fluoride, 10 µg each of leupeptin and aprotinin per ml). For measuring Raf-1 kinase activity in Sf9 cells in the experiments represented in Fig. 4, 5B, and C, and 6A, NP-40 LB was substituted with radioimmunoprecipitation assay (RIPA) buffer (20 mM Tris [pH 8.0], 137 mM NaCl, 10% [vol/vol] glycerol, [vol/vol] NP-40, 0.1% [wt/wt] SDS, 0.5% sodium deoxycholate, 2 mM EDTA). Cell lysates were cleared by centrifugation at 4°C for 15 min. The protein concentration was measured with a kit from Bio-Rad and normalized for all samples in each individual total Western or immunoprecipitation (IP) experiment. Equivalent aliquots of cleared supernatants were mixed with Laemmli SDS-loading buffer (25 mm Tris [pH 6.8], 1% SDS, 2.5% β-mercaptoethanol, 0.5 mg of bromophenol blue per ml, 5% glycerol), separated by SDS-PAGE, and transferred to a Hybond-ECL membrane (Amersham). Following preclearing, IP was performed for 2 h at 4°C, using 0.5 μg of purified anti-FLAG, anti-c-Myc, anti-HA monoclonal antibody or indicated purified rabbit polyclonal antisera. Immune complexes were then recovered by binding to GammaBind-Plus Sepharose (Pharmacia). Alternatively, GST fusion proteins were purified using pre-equilibrated GSH-Sepharose (Pharmacia) as described elsewhere (64). After three washes with 50 volumes lysis buffer, GSH-Sepharose-bound proteins and immunocomplexes were processed for electrophoresis as described above. The entire protein purification procedure was done at 4°C. Immunoblot detection was performed with specified antibodies in 5% dried milk in phosphate-buffered saline and developed as described by the manufacturer of the enhanced chemiluminescence (ECL) system (Amersham). For reblotting, membranes were incubated in 20 mM DTT-1% SDS in phosphate-buffered saline for 10 min at ambient temperature

Protein purification and in vitro association assays. GST fusion proteins were produced and purified by GSH-Sepharose affinity chromatography in NETN buffer (20 mM Tris. [pH 8.0], 0.1 M NaCl, 1 mM EDTA, 0.5% NP-40) supplemented with proteinase and phosphatase inhibitors as previously described (64). Kinase-defective bacterial Hise Mek-1 (K97M) was similarly prepared, using a kit from Qiagen. FLAG-p50^{cdc-37} was immunoaffinity purified by agarose-cross-linked anti-FLAG monoclonal antibody M2 (Kodak) according to the supplier's instructions. For studying in vitro associations, GSH-Sepharose-bound GST fusion proteins were then directly incubated with either purified or in vitro-translated proteins in NETN buffer for 2 h at 4°C. Bound complexes were subsequently washed three times in 50 volumes of prechilled NETN buffer, and after SDS-PAGE they were either immunoblotted or, for [35S]methionine-labeled proteins, directly analyzed by fluorography.

Protein kinase assays. For kinase reactions, GSH-Sepharose-bound GST fusion proteins or immunocomplexes, prepared as described above, were addition-

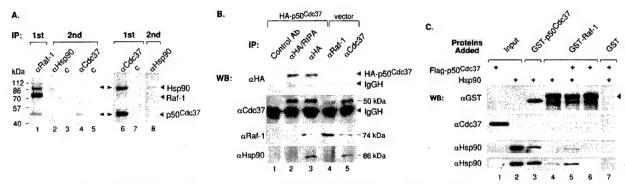


FIG. 1. Association of p50°cdc37, Hsp90, and Raf-1 in vivo and in vitro. (A) Lane 1, anti-Raf-1 IP from [35S]methionine-labeled Cos-1 cells. Lanes 2 to 5, after the primary anti-Raf IP was boiled for 2 min in the presence of 0.5% SDS, a second IP was carried out with anti-Hsp90 or control (c) antibody (lanes 2 and 3) or with polyclonal anti-p50°cdc37 or nonimmune rabbit (c) antibody (lanes 4 and 5, respectively). Lanes 6 and 7, anti-p50°cdc37 primary IPs and nonimmune rabbit serum IPs, respectively, from [35S]methionine-labeled Cos-1 cells. A second IP with anti-Hsp90 antibody (lane 8) was performed with a fraction of the anti-p50°cdc37 primary immunoprecipitate identical to that run in lane 6. The relative migration of molecular weight marker proteins is indicated. (B) Plasmids pMT3-HA-p50°cdc37 and pMT3-HA were transiently transfected into Cos-1 cells, and extracts were immunoprecipitated with anti-FLAG antibody (Ab) M5 as a control (lane 1) or anti-Ha monoclonal antibody 12CA5 under either denaturing or mild conditions (RIPA or NP-40 LB buffer; lanes 2 and 3, respectively) or, to purify endogenous Raf-1 and p50°cdc37 proteins, with anti-Raf-1 (lane 4) and anti-p50°cdc37 (lane 5) monoclonal antibodies. Immunoprecipitated proteins were examined by Western blotting (WB) and ECL for the presence of transfected HA-p50°cdc37 with anti-HA antibody or for the presence of both transfected and endogenous p50°cdc37 with anti-HA antibody or for the presence of both transfected and endogenous p50°cdc37 with anti-HA antibody or for the presence of both transfected and endogenous p50°cdc37 with anti-HA antibody or for the presence of both transfected and endogenous p50°cdc37 with anti-HA antibody or for the presence of both transfected and endogenous p50°cdc37 with anti-HA antibody or for the presence of both transfected and endogenous p50°cdc37 with anti-HA antibody or for the presence of both transfected and endogenous p50°cdc37 with anti-HA antibody or for the presence of both transfected and endogenous p50°cdc37 with a

ally washed in 50 volumes of kinase buffer (25 mM HEPES [pH 7.5], 10 mM MgCl₂, 10 mM MnCl₂, 1 mM DTT), drained, and incubated for 15 min at 30°C in 30 μ l of fresh kinase buffer containing 20 μ M ATP, 5 μ Ci of [γ - 32 P]ATP (6,000 C)/mmol; NEN), and 0.5 μ g of recombinant kinase-defective His₆-Mek-1(K97M). Assays were terminated by the addition of Laemmli SDS-loading buffer, the boiled samples were resolved by SDS-PAGE, and phosphorylated substrate proteins were quantitated by phosphorimager analysis and autoradiography.

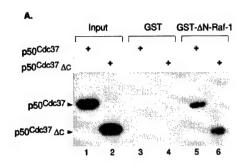
RESULTS

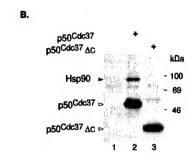
p50^{cdc37} bridges Hsp90 to Raf-1. Previously Hsp90 and p50^{cdc37} were detected by immunological methods in a complex with Raf-1 (51, 66, 78). Here we have used cloned p50^{cdc37} and Raf-1 proteins to reconstitute and further characterize the precise interactions among p50^{cdc37}, Hsp90, and Raf-1. Cos-1 cells express Raf-1, which is the principal Raf isoform (16), and both Hsp90 and p50^{cdc37}. In accordance with previous findings for other tissues (11, 12, 34, 78), two proteins of approximately 90 and 50 kDa coprecipitate with endogenous Raf-1 in Cos-1 cells (Fig. 1A). Subsequent disruption of the complex and a second round of IP with anti-Hsp90 and anti-p50^{cdc37} antisera indicates that these two coprecipitating proteins are immunologically related to Hsp90 and p50^{cdc37}, respectively (Fig. 1A, lanes 1 to 5). The converse experiment precipitating first with anti-p50^{cdc37} antibodies shows stoichiometric coimmunoprecipitation with Hsp90 but reveals only a faint Raf-1 band at the expected 74-kDa range (lanes 6 to 8). This is probably due to the fact that although a significant proportion of Raf-1 protein is bound to p50cdc37 and Hsp90 (19a, 34, 60, 78), only a fraction of p50^{cdc37}, which is present in excess over Raf-1 (not shown) and Hsp90 (1 to 2% of total cytosolic protein), is in a complex with the kinase. Our findings with [35S]methionine-labeled proteins (Fig. 1A, lanes 6 to 8) and by silver staining (not shown) indicate that Hsp90 copurifies in approximately equimolar quantities with p50^{cdc37} and that the p50^{cdc37}-Hsp90 interaction also occurs in vitro in the absence of other proteins

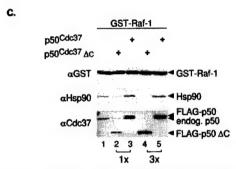
That the cloned p50cdc37 protein indeed associates with

Raf-1 is further supported by the experiments presented in Fig. 1B. HA-p50^{cdc37} or vector plasmids were transiently transfected into Cos-1 cells, and extracts were immunoprecipitated with anti-FLAG antibody M5 as a control (lane 1) or anti-HA monoclonal antibody 12CA5 under either denaturing or mild conditions (RIPA or NP-40 LB buffer; lanes 2 and 3, respectively) or, to purify endogenous Raf-1 and p50^{cdc37} proteins, with anti-Raf-1 (lane 4) or anti-p50^{cdc37} (lane 5) monoclonal antibodies. Immunoprecipitated proteins were then examined by Western blotting and ECL for the presence of transfected HA-p50^{cdc37} or endogenous p50^{cdc37} with anti-HA antibody and anti-p50^{cdc37} rabbit antisera, respectively. Endogenous Hsp90 or Raf-1 proteins were detected with rat-anti-Hsp90 and rabbit-anti-Raf-1 antibodies. In both situations, 50-kDa proteins were found in complex with endogenous Raf-1 and Hsp90. p50^{cdc37}'s associations were sensitive to RIPA buffer (lane 2) and were specific, in that no Hsp90 or Raf-1 could be observed in control antibody IPs (lane 1). Conversely, anti-Raf-1 IPs, followed by Western blotting analysis, identified both p50^{cdc37} and Hsp90 at lower levels, but in a reproducible manner, to copurify with endogenous Raf-1. Thus, by its size and characteristics of its interaction with Raf-1 and Hsp90. cloned p50^{cdc37} is most likely pp50, the previously described 50-kDa Hsp90 partner present in the Raf-1 IPs along with Hsp90.

Similar conclusions were reached in vitro, using combinations of purified Hsp90 and p50^{cdc37} proteins to reconstitute these associations (Fig. 1C). To test whether posttranslationally unmodified Raf-1 can bind to Hsp90 and p50^{cdc37}, GSH-Sepharose-bound GST-Raf-1 that had been produced in *E. coli* was allowed to associate either with p50^{cdc37} or Hsp90 alone or with a mixture of the two proteins. Both p50^{cdc37} and Hsp90 (purified to apparent homogeneity, as judged by silver staining) were found to interact directly and independently with recombinant Raf-1 in vitro (Fig. 1C, bottom panel). Notably, Hsp90's association with Raf-1 greatly increased when p50^{cdc37} was present. This result suggests that Hsp90's associ-







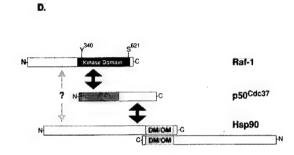


FIG. 2. The N-terminal half of p50°dc37 mediates association with the catalytic domain of Raf-1 but is impaired for Hsp90 interaction and accumulation to Raf-1. (A) Plasmids pSG5-p50°dc37 and pSG5-p50°dc37 cere transcribed and translated in vitro, using T7 RNA polymerase and a reticulocyte lysate system (Promega); 5 μl of each reaction mixture was either analyzed directly (input lanes) or assayed in vitro for binding to either GST or bacterially purified GST-ΔN-Raf-1(Δ26-309) and visualized by SDS-PAGE and fluorography. Comparable results were obtained with full-length GST-Raf-1 (not shown). (B) Cos-1 cells transfected with pSG5-FLAG vector, pSG5-FLAG-p50°dc37, and pSG5-FLAG-p50°dc37, are also indicated. (C) Two micrograms of pEBG-GST-Raf-1 was cotransfected with 5 μg of pSG5-FLAG vector (lane 1), pSG5-FLAG-p50°dc37 (lanes 2 and 3), or pSG5-FLAG-p50°dc37/AC (lanes 4 and 5) at 5 or 15 μg as indicated. After 48 h in DMEM-FBS, all five cultures were harvested and lysed in NP-40 LB, and GST-Raf-1 was GSH-Sepharose purified and tested for associated p50°dc37 or Hsp90 proteins with rabbit anti-p50°dc37 or rat anti-Hsp90 antibody. A control anti-GST immunoblot was also included to detect overexpressed GST-Raf-1 (top panel). (D) Diagram indicating regions of interaction between p50°dc37, Raf-1, and Hsp90. The N-terminal half of p50°dc37 (gray area) which corresponds to p50°dc37ΔC is sufficient for interacting with the C-terminal kinase domain of Raf-1, while its C-terminal half mediates Hsp90 interaction (indicated by black arrows). A distinct weak interaction of Raf-1 directly with Hsp90 through as yet unidentified domains is also proposed and is indicated by the gray arrow. Relative positions of the Y340 and S621 phosphorylation sites present on Raf-1 are also indicated. Since Hsp90 can aboth homodimerize and form oligomers through its C terminus (DM/OM) (41, 48, 49), higher

ation with Raf-1 is induced by a p50^{cdc37}-mediated Raf-1 conformational change or that, more likely, the enhanced association between Raf-1 and Hsp90 (lane 5) is mediated by p50^{cdc37} acting directly to recruit Hsp90 to Raf-1. In the latter scenario, the existence of two distinct sites on Hsp90, one for associating with the Raf-1 bound p50^{cdc37} and a second for directly binding to Raf-1, can be envisioned (Fig. 2D). These experiments demonstrate that recombinant p50^{cdc37} and Hsp90 associate directly and stably with Raf-1, confirming earlier conclusions reached by immunological means (51, 60, 66, 78). Notably, relative to the in vivo situation, Raf-1 association with p50^{cdc37} Raf-1 association with p50^{cdc37} is rather modest, suggesting that modifications such as phosphorylation or association with other proteins may regulate the Raf-1 interaction with p50^{cdc37} and Hsp90 as is the case for its association with 14-3-3 (42).

Since the catalytic C-terminal half of Raf-1 has been reported to be sufficient for interaction with pp50 (66), we tested whether recombinant p50 cdc37 binds to the same Raf-1 region. In vitro-translated p50 cdc37 bound efficiently to immobilized GST- Δ N-Raf-1, a viral Raf form-like construct (3, 63), but not

to GST alone (Fig. 2A) or to the N-terminal Raf-1 regulatory domain alone (not shown). This interaction of p50 cdc37 with Raf-1 occurs via the N-terminal half of p50 cdc37 , as a deletion mutant (p50 $^{cdc37}\Delta$ C) truncated at Met164 to half the original size is sufficient to interact strongly with GST- Δ N-Raf-1. Interestingly, p50 $^{cdc37}\Delta$ C is severely compromised in its ability to associate with Hsp90 in transfected Cos-1 cells (Fig. 2B) compared with full-length p50 cdc37 which readily associates with its chaperone partner.

We then sought to determine whether this mutant could disrupt the Hsp90–Raf-1 association in a dominant fashion. When p50^{cdc37}ΔC was further coexpressed in Cos-1 cells with GST-tagged Raf-1, endogenous Hsp90 association to Raf-1 was strongly inhibited in a dose-dependent manner, with increasing amounts of p50^{cdc37}ΔC binding to the kinase (Fig. 2C). In contrast, overexpressed wild-type p50^{cdc37} not only binds to Raf-1 but also recruits Hsp90 to the complex, in agreement with results of the in vitro experiment shown in Fig. 1C. A likely interpretation of this observation is that overexpressed p50^{cdc37}ΔC competes with endogenous p50^{cdc37} for binding to Raf-1 and that the subsequent Hsp90 association

with GST–Raf-1, which largely depends on intact p50^{cdc37}, is prevented (Fig. 2C; compare lanes 1, 3, and 5). Thus, although some direct Hsp90 binding to Raf-1 cannot be ruled out (Fig. 1C, lane 4), we conclude that the p50^{cdc37} greatly potentiates Hsp90 accumulation into the Raf-1 complex (Fig. 2D) most likely by bridging Hsp90 to Raf-1. This result also suggests that p50^{cdc37} Δ C might interfere with the function of Hsp90 in the Raf-1 complex and potentially acts as a dominant negative allele of p50^{cdc37} in functional assays (described below).

Inability of Raf-1 to respond to serum activation correlates with its inability to complex with p50cdc37-Hsp90 heterodimers. GA, a benzoquinone ansamycin (10), was originally described as a protein kinase inhibitor (74). However, subsequent examination has shown that its effects on kinases are indirect and that it specifically binds to and inhibits the action of Hsp90 (80, 81). GA has been established to be a specific reagent for assessing Hsp90's role in various signaling systems, including v-Src (80), Raf-1 (60, 61), Lck (24), heme-regulated eukaryotic initiation factor 2\alpha kinase (75), and steroid nuclear receptors (31, 65) (reviewed in references 52 and 58). GA competitively displaces ATP and locks Hsp90 into its ADP-specific inactive conformation, disrupting a dynamic equilibrium in which unliganded steroid receptor complexes alternate among various chaperone heterocomplex intermediates (22, 31, 55, 65). GAbound Hsp90 is then unable to form productive complexes with its steroid receptor and kinase targets, which subsequently results in their degradation upon prolonged in vivo GA treatment (59, 60, 62, 80). In an attempt to define the roles of p50^{cdc37} and Hsp90 in Raf-1 kinase heterocomplex formation and activity, we used GA to abrogate Hsp90–Raf-1 association and Raf-1 activation as has been shown by Schulte et al. (60, 61). However, to directly correlate Raf-1's ability to interact with p50^{cdc37} and Hsp90 with its kinase activity, we have designed our experiments to assess the effects of GA on Raf-1 at a stage prior to the time when Raf-1 is depleted from the cells due to prolonged GA treatment. In addition, to improve the detection of associated proteins, we have alternatively used GST fusion cDNAs of Raf-1 or p50cdc37 transiently transfected in mammalian cells. GSH-Sepharose-purified GST-Raf-1 and GST-p50^{cdc37} were then analyzed both for associated proteins and for kinase activity (57, 64).

Cos-1 cells were transfected with either GST-Raf-1 or GST-p50^{cdc37} and replated into three identical cultures. After these cultures were serum starved overnight, two of the replicate transfections were stimulated with 20% serum with or without a 6-h preincubation with GA, as indicated, while the third plate was left untreated. The resulting cellular extracts were analyzed for overall protein expression and protein association with each purified GST-protein. Further, the purified GST-Raf-1 complexes were examined for in vitro kinase activity, using a recombinant kinase-inactive form of Mek-1 as a substrate (Fig. 3A). Western blotting of total cell extracts revealed that expression of the transfected GST-fusion proteins was approximately three times the level of the corresponding endogenous p50^{cdc37} and Raf-1 proteins (not shown) and that under these conditions GA treatment slightly reduced the levels of Raf-1 expression but had no apparent effect on p50^{cdc37} and Hsp90 steady-state levels. From this experiment, the following observations can be made. Consistent with the existing literature, transfected GST-Raf-1 kinase activities was induced by serum but not after GA pretreatment (Fig. 3A). Accordingly, serum stimulation results in small but reproducible enhancement of associations of endogenous p50^{cdc37} and Hsp90 with GST-Raf-1 (Fig. 3B lanes 1 and 2). In contrast, GA pretreatment abolished activation of Raf-1 by serum and almost entirely eliminated this association (Fig. 3B, lanes 3 and

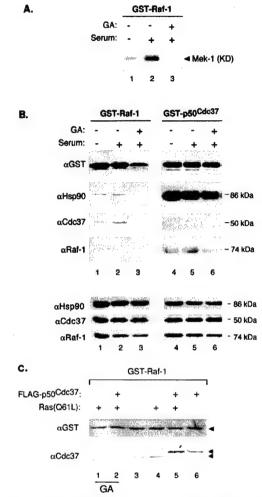


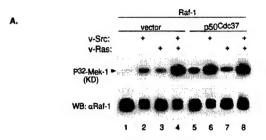
FIG. 3. (A and B) Association of p50cdc37 and Hsp90 with Raf-1 correlates closely with Raf-1 kinase activity. Two micrograms each of pEBG-GST-Raf and pEBG-p50cdc37 were transfected into subconfluent Cos-1 cells, and next day each of the transfected 150-mm-diameter plates was further split into three 100-mm-diameter plates; 16 h later, cultures were fed with serum-free medium for an additional 16 h. GA or only DMSO diluent was then added, followed by serum stimulation as indicated, and the three replicate cultures of each transfection were harvested and solubilized in NP-40 LB. (B, top panels) GST fusion proteins were then purified by GSH affinity chromatography as described in Materials and Methods and analyzed for associated proteins by SDS-PAGE and immunobloting with the indicated antibodies; (A) 0.2-volume extract portions were similarly processed and tested for GST-Raf-1 kinase activity toward recombinant kinase-defective (KD) Mek-1. (B, bottom panels) Control immunoblots of total cell extracts. Control transfections with empty pEBG vector, followed by GSH pull-down assays and Western blotting, showed that no p50cdc37, Hsp90, or Raf-1 associated with the GST propeptide alone (not shown). (C) pEBG-GST-Raf-1 was transfected into Cos-1 cells alone or with pMT2-Ras(Q61L) and pSG5-FLAG-p50cdc37 as indicated; 48 h later, GST-Raf-1 was isolated from NP-40 LB-solubilized cell extracts and tested by Western blotting and ECL for associated endogenous and overexpressed p50cdc37, using anti-Cdc37 antiserum (bottom). Anti-GST blotting was performed to verify levels of GST-Raf-1 expression and recovery. For lanes 1 and 2, GA (2 µg/ml) was included in the growth medium for 6 h before harvest.

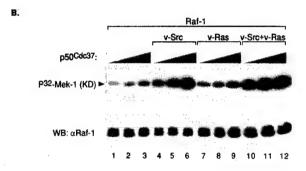
6). Importantly, Raf-1's association with p50^{cdc37}-Hsp90 correlates closely with its activity (Fig. 3B, lanes 1 to 3). Previously, GA was shown to decrease Raf-1 activity and expression in NIH 3T3 cells by destabilizing the protein (60, 61). Note that in this experiment, by assaying Raf-1 levels after a much

shorter treatment of Cos-1 cells with GA, GST-Raf-1 expression is only modestly reduced at this time (Fig. 3B, lanes 3), but both Hsp90 and p50^{cdc37} associations with GST-Raf-1 are nearly abolished. Thus, disruption of the Raf-1-p50^{cdc37}-Hsp90 complex by GA occurs prior to Raf-1 degradation and correlates with the inability of Raf-1 to be activated by serum growth factors even though it remains present in the cell at substantial concentrations. Our results with the p50cdc37ΔC further confirm the requirement for Hsp90 association with Raf-1 independently of effects on Raf-1 protein degradation (see below).

Interestingly, overexpressed GST-p50cdc37 remained sequestered with endogenous Hsp90, and no changes in the association of Hsp90 with GST-p50^{cdc37} were observed under all experimental conditions, including GA pretreatment. Thus, the locking of Hsp90 into the ADP-bound conformation by GA effects the ability of the Hsp90-p50 cdc37 complex to remain associated with Raf-1. Since p50 $^{cdc37}\Delta C$ does not bind Hsp90 but can nevertheless still bind to Raf-1, this finding implies that the GA-bound conformation of Hsp90 inhibits the ability of bound p50^{cdc37} to associate with Raf-1 through either steric hindrance, allosteric regulation, or an indirect mechanism. p50^{cdc37} and Hsp90's respective associations with endogenous Raf-1 also showed small but reproducible serum-mediated enhancement and almost complete elimination by GA (Fig. 3B lanes 4 to 6). Thus, during serum activation of Raf-1, there is a stabilization of p50^{cdc37}-Hsp90-Raf-1 complex formation. A weak associated MAPKKK activity could be detected in GSTp50cdc37 pull-down-in vitro kinase assays from cells coexpressing exogenous Raf-1 (not shown), consistent with both our observation that the bulk of p50^{cdc37} is not Raf-1 associated (Fig. 1A) and the fact that only a small fraction of Raf-1 kinase actually becomes activated during signaling (23, 37, 45). A previous related study (78) using standard antibody-based Raf-1 purification found no changes in endogenous p50cdc37 and Hsp90 coprecipitating with active and inactive transfected Raf-1. The availability of cloned p50^{cdc37}, including a new array of Cdc37-specific antibodies, enabled us to perform reciprocal GST-p50^{cdc37} and GST-Raf-1 pull-down assays. Further, the antibody-free method of isolation allowed us to use higher-stringency GST-protein purification for more accurate assessment of changes in endogenous Raf-1 and p50^{cdc37} complexed with GST-p50^{cdc37} and GST-Raf-1, respectively. This, especially in the case of p50^{cdc37}, which on SDS-PAGE migrates closely with immunoprecipitating antibodies, is, as we also find, technically difficult. We have also observed that coexpression of one GST-tagged protein with a non-GST-tagged version of the other improves further the detection of an increase in Raf-1-p50^{cdc37} association during serum Raf-1 activation (not shown; see Fig. 3C).

In addition to its effects on serum activation of Raf-1, in experiments similar to the one shown in Fig. 3A, we found that GA also inhibits Raf-1 activity driven by cotransfected Ras(Q61L), a constitutively active Ras mutant (not shown). This result indicates that inhibition of Raf-1 by GA occurs downstream of Ras, in agreement with the original observations of Schulte et al. (60, 61), who found that GA had no effect on Ras levels and on Raf-1-Ras-GTP interaction. We have further observed that as with serum induction, activated Ras potentiates Raf-1 association with the p50cdc37 complex (Fig. 3C; compare lanes 3 and 4 and lanes 5 and 6), but in the presence of GA, this association is entirely abolished (lanes 1 and 2) although the p50^{cdc37}-Hsp90 association again remained unaffected (not shown). Altogether, the above results suggest that Raf-1's ability to respond to upstream activating





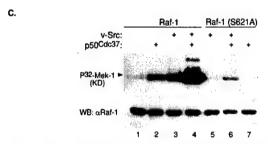


FIG. 4. Sf9 cell coinfection with p 50^{cdc37} results in Raf-1 activation. (A) Baculoviruses encoding Raf-1, v-Src, v-Ras, or p 50^{cdc37} were infected in Sf9 cells in the combinations indicated; 48 h postinfection, Raf-1 was immunoprecipitated with anti-Raf-1 polyclonal antibody C-12 in RIPA buffer and tested for its ability to phosphorylate recombinant kinase-defective (KD) Mek-1 as described in Materials and Methods (top). As controls, kinase assay reactions were also Western blotted (WB) with the same anti-Raf-1 antibody (bottom). (B) Baculovirus coinfection followed by Raf-1 kinase assay (top) and Western blot (bottom) were performed as for panel A. In each set, increasing amounts of p50^{cdc-37} baculovirus (at 1, 3, and 9×) were added as indicated. (C) Wild-type Raf-1 and Raf-1(S621A) were either expressed alone or coexpressed with indicated v-Src or p50cdc37 baculovirus constructs, immunorecipitated and assaued for in vitro baculovirus constructs, immunoprecipitated, and assayed for in vitro kinase activity as for panel A.

stimuli correlates with its ability to form heterotrimeric complexes with p $50^{cdc^{37}}$ and Hsp90.

Activation of Raf-1 by p $50^{cdc^{37}}$ overexpression. The Sf9 in-

sect cell-baculovirus expression system is currently the most widely used in vivo system for evaluating potential Raf-1 activators (reviewed in references 43 and 44). Therefore, we used this system to further analyze the possible involvement of p50 cdc37 in the Raf-1 activation process. Baculoviruses expressing full-length p50 cdc37 and Raf-1, together or in triple combinations with v-Src- or v-Ras-expressing baculoviruses (Fig. 4A), were used to coinfect Sf9 cells. At 48 h postinfection, Raf-1 was immunoprecipitated from Sf9 cells in RIPA buffer and subsequently assayed for its ability to phosphorylate inac-

tive recombinant Mek-1. Consistent with previous reports (reviewed in reference 44), v-Src and, to a lesser extent, v-Ras both activate Raf-1, an effect most prominent when the two oncoproteins are coexpressed (Fig. 4A, lanes 1 to 4). Surprisingly, p50cdc37, a unique protein with no apparent kinase or other recognizable enzymatic domain, by itself strongly activated Raf-1 to an even greater extent than v-Ras and almost as well as, although never better than, v-Src. In coinfected combinations, the p50^{cdc37}-v-Src effect was synergistic (compare lanes 2, 5, and 6), but only modest cooperation was observed between p50 cdc37 and v-Ras (lanes 3 and 7). The cooperation of p50 cdc37 with v-Src and its dose-dependent activation of Raf-1 are shown even more clearly in the dose-response experiment shown in Fig. 4B.

Ser621 of Raf-1 is an indispensable major phosphorylation site whose deletion (25) or substitution by either alanine or even negatively charged aspartate inactivates the protein (17, 46), possibly by compromising the activationcompetent conformation of the Raf-1 catalytic domain (44). Neither v-Src nor p50^{cdc37} could substantially induce Raf-1(S621A) activation compared with the strong positive effect of each on wild-type Raf-1 (Fig. 4C, lanes 5 to 7). Interestingly, however, p50^{cdc37} also enhanced the weak effect of v-Src on the Raf-1 mutant as it did for wild-type Raf-1 (lanes 4 and 6). This result suggests that p50^{cdc37}, in conjunction with its more abundant partner Hsp90, may be rate limiting in insect cells under these conditions and act as a chaperone by increasing the proportion of Raf-1 which is in the active conformation

Inhibition of Raf-1 activation by dominant negative p50cdc37 and GA. Since the deletion mutant p50 $^{cdc37}\Delta$ C fails to bind to both mammalian and insect Hsp90, we sought to determine whether this mutant might interfere with Raf-1 activity by displacing the wild-type insect p50^{cdc37}-Hsp90 complex from Raf-1 since it retains the ability to bind to Raf-1 (Fig. 2). In the experiment shown in Fig. 5A, we attempted to correlate the effects of p50 $^{cdc37}\Delta$ C on Raf-1 activity with its aforementioned ability to displace the full-length p50cdc37 protein upon overexpression (Fig. 2C). Previously it has been found that endogenous insect Hsp90 and p 50^{cdc37} associate with overexpressed mammalian Raf-1 in Sf9 cells (11, 12). However, since our $p50^{cdc37}$ antibodies fail to recognize $p50^{cdc37}$ from insect cells, Sf9 cells were coinfected with baculoviruses expressing mammalian p50^{cdc37} and Raf-1 alone or with increasing amounts of a baculovirus expressing p $50^{cdc37}\Delta C$. Extracts of infected cells were then immunoprecipitated with anti-Raf-1 and analyzed for associated mammalian p50^{cdc37} proteins and Hsp83, the endogenous insect homologue of Hsp90 (8), as well as for Raf-1 kinase activity. Figure 5A shows that, as we had previously observed in mammalian cells (Fig. 2C), p50 $^{cdc37}\Delta\dot{C}$ efficiently and in a dose-dependent manner displaced its fulllength counterpart from Raf-1 in coinfected Sf9 cells and strongly reduced the association of insect Hsp90 with Raf-1. The dissociation of p50^{cdc37} and Hsp90 from Raf-1 correlated closely with the reduction of Raf-1 activation to basal levels (Fig. 5A, top). A control Western blot of total cellular extracts from this experiment indicates that this effect was not due to decreased expression of wild-type p50 cdc37 , endogenous Hsp90, or Raf-1 kinase (Fig. 5A). We conclude that p50 $^{cdc37}\Delta C$ functions a dominant negative for the p50 cdc37 -mediated Raf-1p50^{cdc37}-Hsp90 complex formation and subsequent Raf-1 kinase activation.

We also examined whether p50cdc37ΔC could inhibit Raf-1 activation by Ras and v-Src and again found that overexpression of p $50^{cdc37}\Delta C$ in insect cells abrogated Raf-1 activation by oncogenic Src and Ras (Fig. 5B). Thus, activation of Raf-1 by

both v-Src and v-Ras in Sf9 cells is dependent on the ability of $p50^{cdc^{37}}$ and Hsp90 to form a productive complex with Raf-1 kinase. To gain more insight into the mechanism of p50cdc37 dependent Raf-1 activation, we assessed the effects of wildtype and dominant negative p50cdc37 on the activity of Raf-1 catalytic domain site mutants by coinfection of Sf9 cells. As expected, Raf-1(K375M), which is kinase inactive (14), could not be stimulated by $p50^{cdc37}$ or Src (not shown). Tyr340 and to a lesser extent Tyr341 have previously shown to be important regulatory sites, whose phosphorylation by tyrosine kinases presumably activates Raf-1 by interfering with negative regulation of the catalytic domain by the amino terminus of the protein (14). Since, as shown above, p50cdc37 binds both in vivo and in vitro to the catalytic half of the Raf-1 protein and interacts also both physically and functionally with Src kinases (references 4 and 13 and data not shown), we reasoned that p50^{cdc37}'s role might be auxiliary to tyrosine kinase function, i.e., by facilitating or promoting Raf-1 tyrosine phosphorylation or by preserving the active Raf-1 conformation. To test this, we coexpressed in Sf9 cells p50^{cdc37} along with Raf-1(Y340D), a constitutively active mutant (14). Indeed, p50^{cdc37}, s coexpression with Raf-1(Y340D) (Fig. 5C), even at the highest possible amounts (not shown), failed to further superinduce the already high basal activity of this mutant, consistent with the above-hypothesized role for p50 cdc37 . However, when we also tested the effect of p50 $^{cdc37}\Delta$ C on Raf-1(Y340D), we found again the previously noted strong inhibition of Raf-1 activity (Fig. 5C). Consistent with this, we have found that both p50 cdc37 and p50 $^{cdc37}\Delta$ C associate with Raf-1(Y340D), as judged by examination of the coexpressed proteins (not shown). The above results argue strongly for a potential dual role of p50^{cdc37} and its Hsp90 chaperone cofactor in the Raf-1 activation process: one where p50^{cdc37}-Hsp90 might be involved both in the efficient activation of Raf-1 and a second involving maintenance of the active kinase conformation, once relief from repression by the N-terminal domain is achieved either through tyrosine phosphorylation by v-Src (Fig. 4) or by activation of amino acid mutations (Fig. 5C).

Using a complementary experimental approach, we then tested whether GA-mediated inhibition of insect cell Hsp90 would abrogate baculovirus Raf-1 activation as we had observed in Cos-1 cells. Indeed, GA treatment of Sf9 cells coinfected with Raf-1 and viruses expressing v-Src, v-Ras, or p50^{cdc37} resulted in dramatic decreases in Raf-1 activity (Fig. 6A) that correlated with a substantial loss of endogenous Hsp90 binding to Raf-1 in all tested combinations (Fig. 6B and data not shown). It is of note that under the conditions used, GA resulted in only slight depletion in Raf-1 protein, which, interestingly, exhibited a noticeable mobility up-shift during SDS-PAGE. Thus, the dramatic reduction in Raf-1 kinase activity cannot be accounted for by changes in levels of Raf-1 protein expression (control anti-Raf-1 immunoblot in Fig. 6A). As we have additionally observed, coexpression of Raf-1 with Hsp90 deletion constructs also abrogate Raf-1 activation without causing Raf-1 protein degradation (data not shown). Thus, Raf-1 activation by coexpression with p50cdc37, v-Src, or v-Ras is dependent in each case on functional endogenous insect Hsp90.

We then examined whether, as previously found for Cos-1 cells, the GA inhibitory effect in Sf9 cells could be due to disruption of complex formation between Raf-1 and p50cdc37-Hsp90. In agreement with both in vitro (Fig. 1C) and in vivo reconstitution data for Cos-1 cells (Fig. 2C), the results in Fig. 6B show that coexpression of mammalian p50^{cdc37} with Raf-1 in Sf9 cells results in strong p50^{cdc37}-Raf-1 complex formation

and enhanced recruitment of endogenous Hsp90 into the ki-

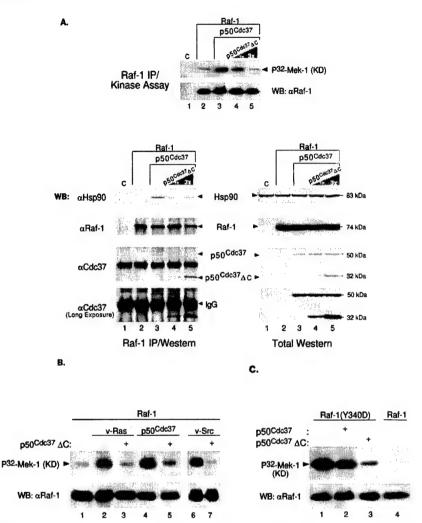


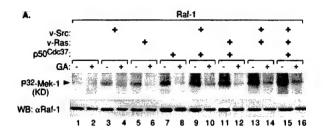
FIG. 5. p50°cdc37ΔC disrupts Raf-1-p50°cdc37-Hsp90 complex formation and abrogates p50°cdc37-mediated Raf-1 activation. (A) A baculovirus encoding p50°dc37ΔC mutant was coinfected at the same MOI or a threefold greater excess MOI with p50°dc37 (lanes 4 and 5) and Raf-1. Control Sf9 cultures included an empty-vector baculovirus infection (C; lane 1) and cultures infected with Raf-1 alone or in combination with p50°dc37 (lanes 2 and 3, respectively); 48 h postinfection, cells were solubilized in NP-40 LB, and a portion of each of the five extracted cultures was harvested, subjected to anti-Raf-1 IPs under nondenaturing conditions using NP-40 LB (see Materials and Methods), and analyzed either for Raf-1 kinase activity toward kinase-defective (KD) recombinant Mek-1 (top) or for p50°dc37 and Hsp90-associated proteins. For assessment of protein expression, control Western blots (WB) of total cellular extracts are shown on the right. (B and C) p50°dc37 and inhibits v-Src and v-Ras activation of Raf-1. (B) Raf-1 was immunoprecipitated and analyzed for its activity toward recombinant inactive Mek-1 from Sf9 cells coinfected with the indicated baculoviruses as described for Fig. 4A. The effect of v-Src (lanes 6 and 7) was examined in a separate experiment involving a shorter kinase assay exposure. (C) The effect of p50°dc37 and is shown in lane 4.

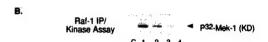
nase complex (compare lanes 1 and 3). This correlates well with p50^{cdc37}-mediated Raf-1 activation as evidenced by the in vitro kinase activity of immunoprecipitated Raf-1 in a parallel assay (Fig. 6B, top panel). However, in GA-treated replicate cultures, both of these effects were almost entirely eliminated. We conclude, therefore, that under all conditions tested in both mammalian and insect cells, Raf-1 must be able to efficiently complex with both p50^{cdc37} and Hsp90 in order to achieve and/or maintain its activated state.

p50^{cdc37} contributes to the transduction of EGF signals that

p50^{cdc37} contributes to the transduction of EGF signals that activate the MAPK cascade via Raf-1. Activated Raf-1 transduces signals to multiple pathways. The best-studied of these is the MAPK pathway. If, therefore, the association of the p50^{cdc37}-Hsp90 complex with Raf-1 contributes to the activa-

tion of Raf-1, the dominant negative mutant p50 $^{cdc37}\Delta C$, which disrupts this complex, would be expected to interfere with the transduction of physiological signals from Raf-1 to the MAPK cascade. To test this hypothesis, we overexpressed p50 $^{cdc37}\Delta C$ or its full-length p50 cdc37 counterpart in combination with Raf-1 in Cos-1 cells, using the Targefect high-efficiency transfection system. Duplicate serum-starved cultures were harvested with or without EGF stimulation, and solubilized cell extracts were then examined by Western blotting with an antibody against activated phospho-MAPK or with control antibodies against transfected Raf-1 or p50 cdc37 (Fig. 7). The results revealed that in contrast to the wild-type protein (Fig. 7, lanes 3 and 4), transfected p50 $^{cdc37}\Delta C$ inhibited EGF-stimulated Raf-1 activation as judged by Raf-1 kinase assay (not





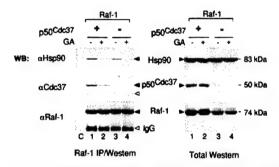


FIG. 6. GA inhibits Raf-1 activation in Sf9 cell by disrupting Raf-1–Hsp90-p50^{rdc37} complex formation. (A) Raf-1 alone or in combination with v-Src, v-Ras, or p50^{rdc37} was expressed in Sf9 cells, incubated for 48 h, immunoprecipitated with anti-Raf-1 polyclonal antisera in RIPA buffer, and tested for in vitro kinase activity. Even-numbered lanes represent parallel cultures treated with GA (2 µg/ml) for 4 h before being harvested and analyzed similarly. Blotted kinase reactions (top panel) were tested for immunoprecipitated Raf-1 protein levels, using rabbit anti-Raf-1 Western blotting (WB) (bottom). Note that GA-treated Raf-1 migrates slower than nontreated samples (bottom) and is severely deficient in phosphorylating recombinant kinase-defective (KD) Mek-1 (top panel). (B) Sf9 cell cultures coinfected with Raf-1 and p50^{rdc37} or empty-vector baculovirus were each split into two replicate cultures 24 h postinfection; 24 h later, one replicate culture was treated with GA (2 µg/ml) for 2 h while the other was similarly treated with only DMSO diluent as indicated. Cell extracts in NP-40 LB were subjected to Raf-1 IP followed by Raf-1 kinase assay (top panel) or Western blot analysis (bottom left) or, additionally, directly analyzed for respective Raf-1, p50^{rdc37}, or Hsp90 protein expression (lane C is like lane 3 except that immunoprecipitating Raf-1 antibody was omitted.) Open arrowheads denote positions of immunoprecipitating anti-Raf-1 antibodies.

shown) and subsequent MAPK activation as determined by detection of dually phosphorylated endogenous Erk-2 with anti-phospho-Erk antibodies (lanes 5 and 6). Thus, not only is the p50cdc37 C-terminal mutant unable to support Raf-1 activation, but it also prevents Raf-1-mediated downstream signaling through the MAPK pathway. Thus, GA and p50cdc37 Δ C, which target the Hsp90 and p50cdc37 components of the Raf-1 activation complex, respectively, produce similar adverse effects: disruption of the native Raf-1 heterocomplex, inhibition of Raf-1 activation, and interruption of signaling to downstream Raf-1 effectors. These findings show that the p50cdc37-Hsp90 complex contributes to the activation of Raf-1 by growth fac-

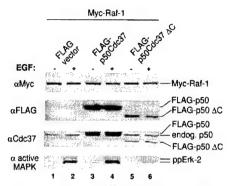


FIG. 7. Dominant negative $p50^{cdc37}$ inhibits MAPK activation. Cos-1 cells transiently transfected by using Targefect with pMT2-Raf-1 and $p50^{cdc37}$ or $p50^{cdc37}\Delta C$, or with vector alone, were split; one set of duplicates was serum starved, while the other was stimulated with EGF. Solubilized extracts were then analyzed either with anti-active-Erk rabbit antiserum (bottom) or for levels of expression with the indicated antibodies (top three panels).

tors and plays a critical role in the transduction of growth factor-generated Raf-1 signals to the MAPK pathway.

DISCUSSION

Based on observations that both Hsp90 and p50^{cdc37} copurify with various protein kinases, it has been proposed that these two proteins comprise a complex that regulates kinase conformation and activity (4, 28, 53). However, this hypothesis has yet to be examined biochemically. The recent cloning of p50^{cdc37} has allowed us to directly investigate the role of the p50^{cdc37}-Hsp90 complex in the regulation of the Raf-1. We have found that coexpression of p50^{cdc37} with Raf-1 leads to Raf-1 activation and that disruption of the p50^{cdc37}-Hsp90 heterodimer interaction with Raf-1 by either p50^{cdc37}-AC or GA inhibits Raf-1 activation and signaling through Erk. These results indicate that the concerted action of p50^{cdc37} and Hsp90 on Raf-1 plays a critical role in cell signaling via the Raf-1/Mek/Erk pathway.

Although it has previously been hypothesized that Hsp90 brings p50^{cdc37} into a complex with Raf and Src (29, 67, 79), our analysis indicates that Raf-1–Hsp90 association is for the most part p50^{cdc37} dependent and that p50^{cdc37} is the factor which primarily mediates the Raf-1–p50^{cdc37}–Hsp90 complex formation. More specifically, p50^{cdc37} binds to the catalytic domain of Raf-1 through its N terminus and tethers Hsp90 to Raf-1 through a second domain located at its C-terminal half (Fig. 2D). This finding is consistent with the observation of Stepanova et al. (69) that p50^{cdc37} accumulates Hsp90 to Cdk4, although in this case there were no clear effects on kinase activity. Further support for our conclusion stated above is given by the observation that p50^{cdc37} \(\Delta \) associates with Raf-1 even though it cannot bind to Hsp90. Moreover, this mutant prevents the accumulation of Hsp90 into the complex by displacing its endogenous full-length counterpart from Raf-1.

Surprisingly, however, GA disrupts the association of the Hsp90-p50^{cdc37} complex with Raf-1 even though it is known to bind only Hsp90 and fails to dissociate the Hsp90-p50^{cdc37} complex itself. This could be explained in several ways. GA is known to competitively displace ATP and, by binding tightly to Hsp90, to lock the chaperone into its ADP-specific inactive conformation (7, 22, 55, 72). This conformation may prevent complex binding by steric hindrance, since most of p50^{cdc37} is bound to Hsp90. p50^{cdc37}ΔC, in contrast, being unable to bind

Hsp90, would be free to associate with Raf-1. Alternatively, p50^{cdc37} may bind to the GA-Hsp90 complex in such a way that it is no longer able to bind to Raf-1. Thus, both Hsp90 and p50^{cdc37} must be in a functional complex in order to form a productive heterotrimeric complex with Raf-1. In general, however, these results validate experimentally the earlier proposal that Hsp90's specific associations might be mediated through Hsp90-associated cofactors and that pp50, in particular, might function in targeting Hsp90 to v-Src and Raf-1 kinases (6, 52, 53). It is notable that Hsp90 and p50^{cdc37} can sometimes function independently of each other. p50^{cdc37} has not been detected in steroid receptor complexes (54), and we have found that Mek-1 forms a tight complex with p50^{cdc37} that

is characteristically devoid of Hsp90 (19a).

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Several lines of evidence indicate that p50cdc37-Hsp90 association with Raf-1 is necessary for the Raf-1 kinase activity. First, overexpressed p50^{cdc37}\(\Delta\)C reduces both Hsp90 association with Raf-1 and Raf-1 kinase activity by competitively displacing wild-type p50^{cdc37} from the Raf-1 complex. Second, GA, an Hsp90-specific inhibitor, blunted Raf-1 activation by serum (Fig. 3), and this inhibition correlated with a dramatic loss of p50^{cdc37}-Hsp90 heterodimers from the kinase. That occupation of the ATP/ADP binding pocket of Hsp90 by GA results in dissociation of the protein from Raf-1 is consistent with the notion that alternating cycles of ATP and ADP binding regulate Hsp90 conformation and, in turn, its ability to mediate the formation of productive signaling heterocomplexes (7, 22, 55, 72). The inhibition by GA was also observed with BXB-Raf-1, a constitutively active N-terminal Raf-1 deletion mutant (3), which consistently binds to p50cdc37 and Hsp90 even more strongly than its full-length counterpart (19a). Coupled with our findings that the vast majority of cytoplasmic p50^{cdc37} is sequestered in heterodimeric complexes by Hsp90 and that it is primarily responsible for bringing Hsp90 into the Raf-1 complex, these results suggest that the interface of p50^{cdc37}-Raf-1 interaction is a target of GA action and that GA-induced conformational alteration of the Hsp90p50^{cdc37} heterodimer either leads to the release of the heterodimer as a whole from Raf-1 or prevents it from rebinding to Raf-1. Freed Raf-1 then becomes subject to accelerated degradation as previously observed by Schulte et al. (60). Interestingly, p $50^{cdc^{37}}\Delta C$ binding to Raf-1 excludes Hsp90 from the complex but does not lead, as GA treatment does, to Raf-1 degradation. p50 $^{cdc37}\Delta$ C further inhibits Raf-1 activation, which also suggests that Hsp90 and p50 cdc37 play an active and positive role in Raf-1 signaling rather than merely serving to stabilize the kinase.

Strikingly, we have found that p50cdc37 itself, upon coinfection in insect cells with Raf-1, results in strong dose-dependent Raf-1 catalytic activity. This activation is even stronger than that observed with v-Ras and only slightly weaker than v-Src-mediated Raf-1 activation. Moreover, p50^{cdc37} was able to enhance the weak v-Src-mediated activation of Raf-1(S621A), a well-characterized conformation-compromised, and thus inactive, Raf-1 mutant. Given that Hsp90, p50^{cdc37}'s partner, is a highly abundant protein, these results suggest that p50cdc37 may be a rate-limiting component under conditions of Raf-1 overexpression and may contribute to the formation or stabilization of the active Raf-1 conformational state. As with v-Src and v-Ras, this effect requires phosphorylatable Ser621 for function (46). In contrast, p50^{cdc37} failed to induce further the already high constitutive activity of Raf-1(Y340D), an N-terminal repression-relieved activated Raf-1 mutant (14). One possible interpretation of this result is that p50^{cdc37} enhances Src-mediated phosphorylation and activation of Raf-1, a notion supported by the observed physical and functional interactions between Src kinases and p50^{cdc37} (reference 4 and unpublished results), including their strong synergistic effect on activating Raf-1 activation (Fig. 4). However, our finding that the dominant negative p50^{cdc37} deletion also down-regulates Raf-1(Y340D) (Fig. 5) in a dose-dependent fashion (not shown) indicates that some of the effects of p50^{cdc37}-Hsp90 complex are independent of tyrosine phosphorylation as well. Thus, it is likely that the p50^{cdc37}-Hsp90 complex is further required to maintain the activated Raf-1 kinase in its active conformation. This latter interpretation would be consistent as well with the findings that activated Ras-independent *Drosophila* Raf alleles still require Hsp90 association for constitutive function at the membrane (76). It is not yet known whether the *Drosophila cdc37* mutation can also suppress this activated Raf allele. This genetic result also indicates that Hsp90 affects Raf-1 activity independently of Raf-1 translocation to the plasma membrane.

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Mere addition of purified p50^{cdc37} and Hsp90 to Raf-1 does not activate the kinase in vitro (unpublished observation). Furthermore, it is worth noting that under commonly used kinase assay conditions, Raf-1, precipitated in RIPA buffer and thus presumably stripped of bound p50^{cdc37} and Hsp90, remains active. This finding suggests that p50^{cdc37} and Hsp90 exert their activation role in vivo in conjunction with additional Raf-1 activation factors and do not need to stay associated with Raf-1 in vitro in order for the kinase to remain active; it also argues against a strictly structural role for the p50^{cdc37}-Hsp90 complex in maintaining Raf-1 activity. This observation may also explain why we can detect only a relatively weak associated MAPKKK activity in p50^{cdc37} immunoprecipitates. As with other chaperone proteins, the p50^{cdc37}-Hsp90 complex may interact with Raf-1 in a transient manner and release after

catalyzing conformational changes in Raf-1.

Previous work in Raf-1 overexpression systems has suggested that there may be a limiting cytosolic factor which is required for maximal Raf-1 activation (5, 26, 36, 70, 78). Our results suggest that p50^{cdc37} could well be a component of this activity. However, since p50 cdc37 is more abundant than Raf-1, the ability of p50 cdc37 overexpression alone to activate endogenous Raf-1 is modest relative to its marked ability to activate coexpressed Raf-1. This finding suggests that in unstimulated cells there may be a stoichiometric inhibitor of Raf-1 signaling whose effects are partially overcome by overexpression of Raf-1. Conceivably, under these conditions, the p50cdc37 Hsp90 complex becomes limiting and overexpressed p50cdc37 complexes with the already abundant Hsp90 to reconstitute the Raf-1-p50^{cdc37}-Hsp90 complex and allow activation of the kinase. That the Hsp90-p50^{cdc37} complex would be limiting in these experiments would also be consistent with a model in which the complex serves as a scaffold for Raf-1 oligomerization. There is evidence both that oligomerization can lead to Raf-1 activation (15, 35) and that Hsp90 forms homodimers and oligomers (40, 41, 48, 49). In further support, most of native Raf-1 is found in large (300- to 500-kDa) complexes with p50^{cdc37} and Hsp90, and it is this form of Raf-1 that becomes membrane activated (78).

An important remaining question is whether the associations or the activity of the p50^{cdc37}-Hsp90 complex are subject to regulation. First, we have found increased formation of the Raf-1-p50^{cdc37}-Hsp90 ternary complex after serum stimulation and in response to activated Ras. It is possible that this contributes to the activation of the small fraction of Raf-1 that is reportedly sufficient for effective signaling. This would be consistent as well with our finding that coexpression of p50^{cdc37} with Raf-1 accumulates Hsp90 and activates Raf-1 in a dose-dependent manner. Analogously, Garcia-Cardena et al. (18)

11. Dent, P., T. Jelinek, D. K. Morrison, M. J. Weber, and T. W. Sturgill. 1995. Reversal of Raf-1 activation by purified and membrane-associated protein phosphatases. Science 268:1902–1906. 12. Dent. P., D. B. Reardon, D. K. Morrison, and T. W. Sturgill, 1995. Regula-

tion of Raf-1 and Raf-1 mutants by Ras-dependent and Ras-independent

mechanisms in vitro. Mol. Cell. Biol. 15:4125-4135.

Dey, B., J. J. Lightbody, and F. Boschelli. 1996. CDC37 is required for p60v-src activity in yeast. Mol. Biol. Cell 7:1405–1417.
 Fabian, J. R., I. O. Daar, and D. K. Morrison. 1993. Critical tyrosine residues

regulate the enzymatic and biological activity of Raf-1 kinase. Mol. Cell. Biol. 13:7170-7179.

Farrar, M. A., I. Alberol, and R. M. Perlmutter. 1996. Activation of the Raf-1 kinase cascade by coumermycin-induced dimerization. Nature 383:178-181.

16. Faure, M., and H. R. Bourne. 1995. Differential effects on cAMP on the MAP kinase cascade: evidence for a cAMP-insensitive step that can bypass Raf-1. Mol. Biol. Cell 6:1025-1035.

17. Ferrier, A. F., M. Lee, W. B. Anderson, G. Benvenuto, D. K. Morrison, D. R. Lowy, and J. E. DeClue. 1997. Sequential modification of serines 621 and 624 in the Raf-1 carboxyl terminus produces alterations in its electrophoretic mobility. J. Biol. Chem. 272;2136–2142.

18. Garcia-Cardena, G., R. Fan, V. Shah, R. Sorrentino, G. Cirino, A. Papapetropoulos, and W. C. Sessa. 1998. Dynamic activation of endothelial nitric oxide synthase by Hsp90. Nature 392:821-824.

Gerber, M. R., A. Farrell, R. J. Deshaies, I. Herskowitz, and D. O. Morgan. 1995. Cdc37 is required for association of the protein kinase Cdc28 with G1 and mitotic cyclins. Proc. Natl. Acad. Sci. USA 92:4651-4655.

19a, Grammatikakis, N. Unpublished data.

20. Grammatikakis, N., A. Grammatikakis, H. Piwnica-Worms, B. P. Toole, and B. H. Cochran. 1996. The cell cycle, p. 72. Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.

21. Grammatikakis, N., A. Grammatikakis, M. Yoneda, Q. Yu, S. D. Banerjee, and B. P. Toole. 1995. A novel glycosaminoglycan-binding protein is the vertebrate homologue of the cell cycle control protein, Cdc37. J. Biol. Chem. 270:16198-16205.

 Grenert, J. P., W. P. Sullivan, P. Fadden, T. A. J. Haystead, J. Clark, E. Mimnaugh, H. Krutzsch, H. J. Ochel, T. W. Schulte, E. Sausville, L. M. Neckers, and D. O. Toft. 1997. The amino-terminal domain of heat shock protein 90 (hsp90) that binds geldanamycin is an ATP/ADP switch domain hat regulates hsp90 conformation. J. Biol. Chem. 272:23843-2350.

23. Hallberg, B., S. I. Rayter, and J. Downward. 1994. Interaction of Ras and Raf in intact mammalian cells upon extracellular stimulation. J. Biol. Chem. 269:3913-3916

Hartson, S. D., E. A. Ottinger, W. Huang, G. Barany, P. Burn, and R. L. Matts. 1998. Modular folding and evidence for phosphorylation-induced stabilization of an hsp90-dependent kinase. J. Biol. Chem. 273:8475-8482.

Heidecker, G., M. Huleihel, J. L. Cleveland, W. Kolch, T. W. Beck, P. Lloyd, T. Pawson, and U. R. Rapp. 1990. Mutational activation of c-raf-1 and definition of the minimal transforming sequence. Mol. Cell. Biol. 10:2503–

Howe, L. R., S. J. Leevers, N. Gomez, S. Nakielny, P. Cohen, and C. J. Marshall. 1992. Activation of the MAP kinase pathway by the protein kinase raf. Cell 71:335-342.

Huang, L., N. Grammatikakis, and B. P. Toole. 1998. Organization of the

chick CDC37 gene. J. Biol. Chem. 273:3598–3603.

Hunter, T., and R. Y. C. Poon. 1997. Cdc37: a protein kinase chaperone?

Trends Cell Biol. 7:157–161.

Hutchison, K. A., B. K. Brott, J. H. De Leon, G. H. Perdew, R. Jove, and W. B. Pratt. 1992. Reconstitution of the multiprotein complex of pp60src, hsp90, and p50 in a cell-free system. J. Biol. Chem. 267:2902-2908

Jakob, U., and J. Buchner. 1994. Assisting spontaneity: the role of Hsp90 and small Hsps as molecular chaperones. Trends Biochem. Sci. 19:205–211.

Johnson, J. L., and D. O. Toft. 1995. Binding of p23 and hsp90 during assembly with the progesterone receptor. Mol. Endocrinol. 9:670-678.

Kimura, Y., S. L. Rutherford, Y. Miyata, I. Yahara, B. C. Freeman, L. Yue, R. I. Morimoto, and S. Lindquist. 1997. Cdc37 is a molecular chaperone with specific functions in signal transduction. Genes Dev. 11:1775–1785.

Lamphere, L., F. Fiore, X. Xu, L. Brizuela, S. Keezer, C. Sardet, G. F. Draetta, and J. Gyuris. 1997. Interaction between Cdc37 and Cdk4 in human

cells. Oncogene 14:1999–2004.

Lovric, J., O. Bischof, and K. Moelling. 1994. Cell cycle-dependent association of Gag-Mil and hsp90. FEBS Lett. 343:15–21.

Luo, Z., G. Tzivion, P. J. Belshaw, D. Vavvas, M. Marshall, and J. Avruch. 1996. Oligomerization activates c-Raf-1 through a Ras-dependent mechanism. Nature 383:181-185.

Marais, R., Y. Light, H. F. Paterson, C. S. Mason, and C. J. Marshall. 1997. Differential regulation of Raf-1, A-Raf, and B-Raf by oncogenic ras and tyrosine kinases. J. Biol. Chem. 272:4378-4383.

Marais, R., and C. J. Marshall. 1996. Control of the ERK MAP kinase

cascade by Ras and Raf. Cancer Surv. 27:101-125.

Marshall, C. J. 1995. Specificity of receptor tyrosine kinase signaling: transient versus sustained extracellular signal-regulated kinase activation. Cell 80:179-185.

have recently found that extracellular regulators of endothelial nitric oxide synthase induce the rapid recruitment of Hsp90 to the enzyme, resulting in its membrane activation. It is also possible that changes in protein association or modifications of preexisting Raf-1-Hsp90-p50^{cdc37} trimeric complexes are sufficient to cause Raf-1 activation or derepression during cell stimulation. Since both p50cdc37 and Hsp90 are phosphoproteins (4, 34, 78, 79), their protein associations within the Raf-1 signalsome could in turn be modulated by phosphorylation. Indeed, phosphorylation-dependent interactions appear to be involved in the regulatory interaction of other kinases with Hsp90, including v-Src (39), Lck (24), and HRI (73, 75). In addition, serum regulation of the phosphorylation state of the Hsp90-p50^{cdc37} complex could play an important role in Raf-1 activation. Alternatively, serum might regulate the nucleotide binding state and conformation of Hsp90 (22, 55, 72) that is associated with p50^{cdc37} and Raf-1 and thereby allosterically regulate its effects on Raf-1. This may occur either through assisting Raf-1 in the conformational transition to the activated state or by allowing it to achieve a configuration where it is competent to respond to upstream activators.

In summary, our findings complement and extend genetic data for Drosophila and indicate that the p50cdc37-Hsp90 chaperone complex is essential for signaling through the MAPK pathway at the level of Raf-1. Interestingly, the fact that Raf-1 (71, 77), Hsp90 (54), and, as verified by both mRNA and protein analyses (8, 19a), p50^{cdc37} all involve ubiquitously expressed proteins points to a potentially universal Raf-1-Hsp90-p50^{cdc37} signaling complex. Future experiments will address both the exact nature of Raf-1 regulation by the p50cdc37-Hsp90 heterodimer and whether additional kinases are similarly modulated.

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REFERENCES

- 1. Avruch, J., X. F. Zhang, and J. M. Kyriakis. 1994. Raf meets Ras: completing the framework of a signal transduction pathway. Trends Biochem. Sci. 19:279-283
- 2. Borkovich, K. A., F. W. Farrelly, D. B. Finkelstein, J. Taulien, and S. Lindquist, 1989, hsp82 is an essential protein that is required in higher concentrations for growth of cells at higher temperatures. Mol. Cell. Biol.
- 3. Bruder, J., G. Heidecker, and U. Rapp. 1992. Serum-, TPA-, and ras-induced expression from Ap-1/Ets-driven promoters requires Raf-1 kinase. Genes
- 4. Brugge, J. S. 1986. Interaction of the Rous sarcoma virus protein pp60src with the cellular proteins pp50 and pp90. Curr. Top. Microbiol. Immunol. 123:1-22
- 5. Chow, Y. H., K. Pumiglia, T. H. Jun, P. Dent, T. W. Sturgill, and R. Jove. 1995. Functional mapping of the N-terminal regulatory domain in the human Raf-1 protein kinase. J. Biol. Chem. **270**:14100–14106.
- Courtneidge, S. A., and J. M. Bishop. 1982. Transit of pp60v-src to the plasma membrane. Proc. Natl. Acad. Sci. USA 79:7117–7121.
- 7. Csermely, P., and C. R. Kahn. 1991. The 90-kDa heat shock protein (hsp-90) possesses an ATP binding site and autophosphorylating activity. J. Biol. Chem. 266:4943-50.
- 8. Cutforth, T., and G. M. Rubin. 1994. Mutations in Hsp83 and cdc37 impair signaling by the sevenless receptor tyrosine kinase in Drosophila. Cell 77:
- Dai, K., R. Kobayashi, and D. Beach. 1996. Physical interaction of mamma-
- lian CDC37 with CDK4. J. Biol. Chem. 271:22030-22034.

 10. DeBoer, C., P. A. Meulman, R. J. Wnuk, and D. H. Peterson, 1970. Geldanamycin, a new antibiotic. J. Antibiot. (Tokyo) 23:442-447.

- Mimnaugh, E. G., P. J. Worland, L. Whitesell, and L. M. Neckers. 1995. Possible role for serine/threonine phosphorylation in the regulation of the heteroprotein complex between the hsp90 stress protein and the pp60v-src tyrosine kinase. J. Biol. Chem. 270:28654–28659.
- Minami, Y., H. Kawasaki, Y. Miyata, K. Suzuki, and I. Yahara. 1991. Analysis of native forms and isoform compositions of the mouse 90-kDa heat shock protein, HSP90. J. Biol. Chem. 266:10099–10103.
- Minami, Y., Y. Kimura, H. Kawasaki, K. Suzuki, and I. Yahara. 1994. The carboxy-terminal region of the mammalian HSP90 is required for its dimerization and function in vivo. Mol. Cell. Biol. 14:1459–1464.
- 42. Morrison, D. 1994. 14-3-3: modulators of signaling proteins? Science 266: 56-57
- Morrison, D. K. 1995. Activation of Raf-1 by Ras in intact cells. Methods Enzymol. 255:301-310.
- 44. Morrison, D. K. 1995. Mechanisms regulating Raf-1 activity in signal trans-
- duction pathways. Mol. Reprod. Dev. 42:507–514.
 45. Morrison, D. K., and R. E. Cutter. 1997. The complexity of Raf-1 regulation. Curr. Opin. Cell Biol. 9:174–179.
- Morrison, D. K., G. Heidecker, U. R. Rapp, and T. D. Copeland. 1993. Identification of the major phosphorylation sites of the Raf-1 kinase. J. Biol. Chem. 268:17309–17316.
- Nathan, D. F., M. H. Vos, and S. Lindquist. 1997. In vivo functions of the Saccharomyces cerevisiae Hsp90 chaperone. Proc. Natl. Acad. Sci. USA 94:12949–12956.
- Nemoto, T., Y. Ohara-Nemoto, M. Ota, T. Takagi, and K. Yokoyama. 1995. Mechanism of dimer formation of the 90-kDa heat-shock protein. Eur. J. Biochem. 233:1-8.
- Nemoto, T., and N. Sato. 1998. Oligomeric forms of the 90-kDa heat shock protein. Biochem. J. 330:989–995.
- Ozaki, T., K. Irie, and S. Sakiyama. 1995. Molecular cloning and cell cycledependent expression of a novel gene that is homologous to cdc37. DNA Cell Biol. 14:1017–1023.
- 51. Perdew, G. H., H. Wiegand, J. P. Vanden Heuvel, C. Mitchell, and S. S. Singh. 1997. A 50 kilodalton protein associated with raf and pp60(v-src) protein kinases is a mammalian homolog of the cell cycle control protein cdc37. Biochemistry 36:3600-3607.
- Pratt, W. B. 1998. The hsp90-based chaperone system: involvement in signal transduction from a variety of hormone and growth factor receptors. Proc. Soc. Exp. Biol. Med. 217:420-434.
- Pratt, W. B. 1993. The role of heat-shock proteins in regulating the function, folding and trafficking of the glucocorticoid receptor. J. Biol. Chem. 268: 21455–21458.
- Pratt, W. B., and D. O. Toft. 1997. Steroid receptor interactions with heat shock protein and immunophilin chaperones. Endocrine Rev. 18:306–360.
- Prodromou, C., S. M. Roe, R. O'Brien, J. E. Ladbury, P. W. Piper, and L. H. Pearl. 1997. Identification and structural characterization of the ATP/ADPbinding site in the Hsp90 molecular chaperone. Cell 90:65–75.
- Reed, S. I. 1980. The selection of S. cerevisiae mutants defective in the start event of cell division. Genetics 95:561–577.
- Sanchez, I., R. T. Hughes, B. J. Mayer, K. Yee, J. R. Woodgett, J. Avruch, J. M. Kyriakis, and L. I. Zon. 1994. Role of SAPK/ERK kinase-1 in the stress-activated pathway regulating transcription factor c-Jun. Nature 372: 704 709
- Scheibel, T., and J. Buchner. 1998. The Hsp90 complex—a super-chaperone machine as a novel drug target. Biochem. Pharmacol. 56:675–682.
- Schneider, C., L. Sepp-Lorenzino, E. Nimmesgern, O. Ouerfelli, S. Danishefsky, N. Rosen, and F. U. Hartl. 1996. Pharmacologic shifting of a balance between protein refolding and degradation mediated by Hsp90. Proc. Natl. Acad. Sci. USA 93:14536–14541.
- Schulte, T. W., M. V. Blagosklonny, C. Ingui, and L. Neckers. 1995. Disruption of the Raf-1-Hsp90 molecular complex results in destabilization of Raf-1 and loss of Raf-1-Ras association. J. Biol. Chem. 270:24585–24588.
- Schulte, T. W., M. V. Blagosklonny, L. Romanova, J. F. Mushinski, B. P. Monia, J. F. Johnston, P. Nguyen, J. Trepel, and L. M. Neckers. 1996. Destabilization of Raf-1 by geldanamycin leads to disruption of the Raf-1–MEK-mitogen-activated protein kinase signalling pathway. Mol. Cell. Biol. 16:5839-5845

- Segnitz, B., and U. Gehring. 1997. The function of steroid hormone receptors is inhibited by the hsp90-specific compound geldanamycin. J. Biol. Chem. 272:18694–18701.
- 63. Silverstein, A. M., N. Grammatikakis, B. H. Cochran, M. Chinkers, and W. B. Pratt. 1998. p50(cdc37) binds directly to the catalytic domain of Raf as well as to a site on hsp90 that is topologically adjacent to the tetratricopeptide repeat binding site. J. Biol. Chem. 273:20090–20095.
- Smith, D. B., and K. S. Johnson. 1988. Single-step purification of polypeptides expressed in Escherichia coli as fusions with glutathione S-transferase. Gene 67:31-40
- Smith, D. F., L. Whitesell, S. C. Nair, S. Chen, V. Prapapanich, and R. A. Rimerman. 1995. Progesterone receptor structure and function altered by geldanamycin, an hsp90-binding agent. Mol. Cell. Biol. 15:6804–6812.
- Stancato, L. F., Y. H. Chow, K. A. Hutchison, G. H. Perdew, R. Jove, and W. B. Pratt. 1993. Raf exists in a native heterocomplex with hsp90 and p50 that can be reconstituted in a cell-free system. J. Biol. Chem. 268:21711– 21716.
- Stancato, L. F., Y. H. Chow, J. K. Owens-Grillo, A. W. Yem, M. R. Deibel, Jr., R. Jove, and W. B. Pratt. 1994. The native v-Raf.hsp90.p50 heterocomplex contains a novel immunophilin of the FK506 binding class. J. Biol. Chem. 269:22157-22161.
- Stanton, V. P., Jr., D. W. Nichols, A. P. Laudano, and G. M. Cooper. 1989.
 Definition of the human Raf amino-terminal regulatory region by deletion mutagenesis. Mol. Cell. Biol. 9:639-47.
- Stepanova, L., X. Leng, S. Parker, and J. Harper. 1996. Mammalian p50^{Cdc37} is a protein kinase-targeting subunit of Hsp90 that binds and stabilizes Cdk4. Genes Dev. 10:1491–1502.
- Stokoe, D., and F. McCormick. 1997. Activation of c-Raf-1 by Ras and Src through different mechanisms: activation in vivo and in vitro. EMBO J. 16:2384–2396.
- Storm, S. M., J. L. Cleveland, and U. R. Rapp. 1990. Expression of raf family proto-oncogenes in normal mouse tissues. Oncogene 5:345–351.
- Sullivan, W., B. Stensgard, G. Caucutt, B. Bartha, N. McMahon, E. S. Alnemri, G. Litwack, and D. Toft. 1997. Nucleotides and two functional states of hsp90. J. Biol. Chem. 272:8007-8012.
- 73. Szyszka, R., G. Kramer, and B. Hardesty. 1989. The phosphorylation state of the reticulocyte 90-kDa heat shock protein affects its ability to increase phosphorylation of peptide initiation factor 2 alpha subunit by the hemesensitive kinase. Biochemistry 28:1435–1438.
- Uehara, Y., Y. Murakami, K. Suzukake-Tsuchiya, Y. Moriya, H. Sano, K. Shibata, and S. Omura. 1988. Effects of herbimycin derivatives on src oncogene function in relation to antitumor activity. J. Antibiot. (Tokyo) 41: 831-834
- Uma, S., S. D. Hartson, J. J. Chen, and R. L. Matts. 1997. Hsp90 is obligatory for the heme-regulated eIF-2alpha kinase to acquire and maintain an activable conformation. J. Biol. Chem. 272:11648–11656.
- van der Straten, A., C. Rommel, B. Dickson, and E. Hafen. 1997. The heat shock protein 83 (Hsp83) is required for Raf-mediated signalling in Drosophila. EMBO J. 16:1961–1969.
- Wadewitz, A. G., M. A. Winer, and D. J. Wolgemuth. 1993. Developmental and cell lineage specificity of raf family gene expression in mouse testis. Oncogene 8:1055–1062.
- Wartmann, M., and R. J. Davis. 1994. The native structure of the activated Raf protein kinase is a membrane-bound multi-subunit complex. J. Biol. Chem. 269:6695–6701.
- Whitelaw, M. L., K. Hutchison, and G. H. Perdew. 1991. A 50-kDa cytosolic protein complexed with the 90-kDa heat shock protein (hsp90) is the same protein complexed with pp60v-src hsp90 in cells transformed by the Rous sarcoma virus. J. Biol. Chem. 266:16436–16440.
- Whitesell, L., E. G. Mimnaugh, B. De Costa, C. E. Myers, and L. M. Neckers. 1994. Inhibition of heat shock protein HSP90-pp60v-src heteroprotein complex formation by benzoquinone ansamycins: essential role for stress proteins in oncogenic transformation. Proc. Natl. Acad. Sci. USA 91:8324–8328.
- Whitesell, L., S. D. Shifrin, G. Schwab, and L. M. Neckers. 1992. Benzoquinonoid ansamycins possess selective tumoricidal activity unrelated to src kinase inhibition. Cancer Res. 52:1721–1728.

p50^{cdc37} Binds Directly to the Catalytic Domain of Raf as Well as to a Site on hsp90 That Is Topologically Adjacent to the Tetratricopeptide Repeat Binding Site*

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Several protein kinases (e.g. pp60src, v-Raf) exist in heterocomplexes with hsp90 and a 50-kDa protein that is the mammalian homolog of the yeast cell cycle control protein Cdc37. In contrast, unliganded steroid receptors exist in heterocomplexes with hsp90 and a tetratricopeptide repeat (TPR) domain protein, such as an immunophilin. Although p50^{cdc37} and TPR domain proteins bind directly to hsp90, p50^{cdc37} is not present in native steroid receptor hsp90 heterocomplexes. To obtain some insight as to how v-Raf selects predominantly hsp90·p50^{cdc37} heterocomplexes, rather than hsp90·TPR protein heterocomplexes, we have examined the binding of p $50^{cdc^{37}}$ to hsp90 and to Raf. We show that p $50^{cdc^{37}}$ exists in separate hsp90 heterocomplexes from the TPR domain proteins and that intact TPR proteins compete for p50cdc37 binding to hsp90 but a protein fragment containing a TPR domain does not. This suggests that the binding site for $p50^{cdc^{37}}$ lies topologically adjacent to the TPR acceptor site on the surface of hsp90. Also, we show that p50cdc37 binds directly to v-Raf, with the catalytic domain of Raf being sufficient. We propose that the combination of exclusive binding of p50cdc37 versus a TPR domain protein to hsp90 plus direct binding of p50^{cdc37} to Raf allows the protein kinase to select for the dominant hsp90-p50^{cdc37} composition that is observed with a variety of protein kinase heterocomplexes immunoadsorbed from cytosols.

A variety of transcription factors and protein kinases have been recovered from cytosols in native heterocomplexes with the abundant, ubiquitous, and essential protein chaperone hsp90¹ (for review, see Refs. 1 and 2). Several other proteins, all of unknown function, have been recovered in steroid receptor hsp90 and protein kinase hsp90 heterocomplexes. Steroid receptor hsp90 heterocomplexes contain one of several

high molecular weight immunophilins or the protein serine/threonine phosphatase PP5 (1). The protein kinase heterocomplexes contain a 50-kDa phosphoprotein that was originally identified as a component of the pp60^{v-src}-hsp90 heterocomplex (for review, see Refs. 3 and 4).

We and others have recently cloned p50 and identified it as the vertebrate homolog of the yeast cell cycle control protein Cdc37 (5–7).² Genetic evidence suggests that Cdc37 is necessary for Src function (8) and for signaling via the sevenless receptor, a protein tyrosine kinase of *Drosophila* (9). The cyclindependent protein kinase Cdk4 is also recovered in heterocomplexes with hsp90 and p50^{cdc37} (6, 10), and we (10) and Stepanova *et al.* (6) have shown that p50^{cdc37} binds directly to Cdk4 as well as to hsp90.

Three high molecular weight immunophilins, FKBP52 (formerly called p59 or hsp56) (11-14), FKBP51 (15-17), and CyP-40 (18, 19), exist in steroid receptor-hsp90 heterocomplexes. Each of the three immunophilins contains three tetratricopeptide repeats (TPRs), which are degenerative sequences of 34 amino acids (20) that are required for binding to hsp90 (21-23). It has been shown that CyP-40 and FKBP52 compete with each other for binding to hsp90 (21, 24), and that these immunophilins exist in independent receptor hsp90 FKBP52 and receptor hsp90 CyP-40 heterocomplexes (24, 25). Another component of steroid receptor heterocomplexes is protein phosphatase 5 (PP5) (26), which contains four TPRs (27). Because the binding of FKBP52 and CyP-40 to hsp90 is competed by fragments of PP5 (28) and CyP-40 (29) comprising the TPR domains, we have proposed that there is a common TPR acceptor site on hsp90 that binds a variety of TPR-containing proteins (29).

Although native receptor-hsp90 heterocomplexes contain one of the TPR domain proteins, they do not contain p50^{cdc37} (30, 31). In contrast, immune-isolated Src·hsp90 (3) and Cdk4·hsp90 (6) heterocomplexes contain p50^{cdc37}, but no TPR protein has been identified. We have shown that v-Raf, a serine/threonine kinase involved in signal transduction, also exists in heterocomplexes with hsp90 and p50^{cdc37} (31). Although v-Raf immune pellets have the ability to bind a small amount of [³H]FK506 in a Raf·hsp90-specific manner (32), it seems clear that the majority of v-Raf·hsp90 heterocomplexes contain p50^{cdc37}.

It is not known how the protein that is being chaperoned by hsp90 (i.e. steroid receptor or protein kinase) determines the composition of the heterocomplex. In this report, we provide evidence that p50cdc37 binds to hsp90 at a site on its surface that is near the binding site for the TPR domain proteins.

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^{313-763-4450.}¹ The abbreviations used are: hsp, heat shock protein; FKBP, FK506 binding protein; CyP, cyclosporin A binding protein; PP5, protein phosphatase 5; TPR, tetratricopeptide repeat; Src, pp60^{v-src}; Hop, hsp organizer protein (also called p60); PAGE, polyacrylamide gel electrophoresis; TBS, Tris-buffered saline; GST, glutathione S-transferase; TES, 2-[[2-hydroxy-1,1-bis(hydroxymethyl)ethyl]amino]ethanesulfonic acid.

² N. Grammatikakis and B. H. Cochran, unpublished results.

Using FLAG-tagged p50^{cdc37} and PP5, we show that p50^{cdc37} exists in separate hsp90 heterocomplexes from the TPR proteins. In addition to binding to hsp90, p50^{cdc37} binds directly to Raf. It is known that, during the process of Raf-hsp90 heterocomplex assembly, Raf is transiently associated with p60 (also called Hop) (33), which binds to hsp90 via its TPRs (34). p60/ Hop is required for assembly of hsp90 heterocomplexes (35), and we show here that p60/Hop competes for the binding of both TPR domain proteins and p50^{cdc37} to hsp90. Our observations are consistent with a model in which dissociation of p60/ Hop from the newly formed Raf-hsp90 complex results in an open region on the surface of the hsp90 dimer that can be occupied by either p50^{cdc37} or a TPR protein. With continued exchange binding of p50^{cdc37} and TPR domain proteins to Raf-associated hsp90, Raf-hsp90-p50^{cdc37} complexes are rapidly selected because p50^{cdc37} also binds directly to Raf.

EXPERIMENTAL PROCEDURES Materials

Untreated rabbit reticulocyte lysate was from Green Hectares (Oregon, WI). 125I-Conjugated goat anti-mouse and anti-rabbit IgGs were from NEN Life Science Products. Goat anti-mouse IgG-horseradish peroxidase conjugate, monoclonal nonimmune IgG and IgM, purified rabbit IgG, monoclonal anti-glutathione S-transferase (GST) clone GST-2 ascites, and purified glutathione S-transferase were from Sigma. The AC88 monoclonal IgG against hsp90 was from StressGen (Victoria, British Columbia, Canada). The 3G3 monoclonal IgM against hsp90, and the anti-cyclophilin 40 (COOH-terminal peptide) antibody were from Affinity Bioreagents (Golden, CO). The anti-FLAG M2 monoclonal IgG, M2-agarose, and the FLAG peptide were from IBI (New Haven, CT). The C-12 rabbit anti-Raf-1 IgG was from Santa Cruz Biotechnology (Santa Cruz, CA). The anti-Raf antiserum prepared against the carboxyl-terminal 12 amino acids of human Raf-1 (34) was kindly provided by Dr. Richard Jove (Moffitt Cancer Center, Tampa, FL). The DS14F5 monoclonal antibody against p60/Hop (36) and Escherichia coli expressing human p60/Hop were kindly provided by Dr. David Smith (University of Nebraska, Omaha, NE). The XR recombinant pGEX-2T plasmid encoding GST-tagged rabbit FKBP52 (37) was kindly provided by Dr. Jack-Michel Renoir (University of Paris, France). The UPJ56 rabbit antiserum against hsp56 (38) was a kind gift from Dr. Karen Leach (The Upjohn Co., Kalamazoo, MI). The rabbit antiserum against hsp70 and hsp90 (39) was generously provided by Dr. Ettore Appella (National Cancer Institute). Rabit antiserum to PP5, purified FLAG-PP5, and the FLAG-tagged TPR domain of rat PP5 were prepared as described previously (26).

Methods

Cell Culture and Cytosol Preparation—Sf9 cells and 3Y1 rat fibroblasts stably transfected with DNA encoding v-Raf (31) were harvested, washed once, suspended in 1 volume of HE buffer (10 mm Hepes, pH 7.4, 1 mm EDTA), and ruptured by Dounce homogenization. Homogenates were centrifuged 15 min at $12,000 \times g$.

Immunoadsorption—Native hsp90 heterocomplexes were immunoadsorbed from 150 µl of rabbit reticulocyte lysate for 2 h at 4 °C with 15 µl of 3G3 antibody prebound to 12 µl of protein A-Sepharose, as described previously (24). Native p60/Hop heterocomplexes were immunoadsorbed from 150 µl of rabbit reticulocyte lysate with DS14F5 antibody against p60 (3%), and FLAG-PP5 or FLAG-p50 was immunoadsorbed with 6 µg of M2 monoclonal antibody against the FLAG epitope. All immunopellets were washed three times by suspension in 1 ml of TEGM buffer (10 mm TES, 50 mm NaCl, 4 mm EDTA, 10% (w/v) glycerol, 20 mm sodium molybdate, pH 7.6), and proteins were resolved by SDS-polyacrylamide gel electrophoresis.

Western Blotting—Immunoblots were probed with 1 μg/ml AC88 for hsp90 (or, in the case of insect hsp90, with 0.1% hsp70/hsp90 antiserum), 0.1% UPJ56 for hsp56, 0.1% PP5 antiserum for PP5, 1 μg/ml M2 monoclonal for the FLAG-proteins, 0.1% DS14F5 for p60/Hop, 0.1% p50 antiserum for p50°cdc37, 0.1% anti-Raf antiserum for v-Raf, 0.1% GST ascites for GST-Raf, or 0.1% anti-cyclophilin 40 for CyP-40. The immunoblots were developed with the appropriate horseradish peroxidase-conjugated and/or ¹²⁶I-conjugated counter antibody. Although immunoblots from individual immunoadsorption or competition binding experiments are presented, the experiments have been performed at least three times and corroborating results obtained by immunoadsorp-

tion of, or competition by, other proteins are usually presented in other panels of the same figure.

Binding of Proteins to Purified hsp90-Rabbit hsp90 was purified from brain cytosol as described by Hutchison et al. (40). Aliquots (30 μ l) of purified rabbit hsp90 (1 mg/ml) were immunoadsorbed to 12-µl pellets of protein A-Sepharose precoupled with 15 μ l of 3G3 antibody. Pellets were washed twice with 1 ml of HE buffer and suspended in Hepes buffer, pH 7.4, plus 0.1% Nonidet P-40 in a final volume of 100 μ l, including 30 µl of the pooled, hsp90-free hydroxylapatite fraction of rabbit brain cytosol containing p60/Hop, PP5, FKBP52, p50^{cdc37}, and CyP-40 prepared exactly as described by Owens-Grillo et al. (29). In experiments where binding of proteins to hsp90 was competed with the PP5 TPR domain, 30 µg of purified FLAG-tagged PP5 TPR in 30 µl of 20 mm Hepes, 1 mm dithiothreitol, 150 mm NaCl were added, maintaining the same final incubation volume of 100 μ l. In experiments where binding of proteins to hsp90 was competed with bacterially expressed p60/Hop, Sf9-expressed FLAG-PP5 or FLAG-p50^{cdc37}, bacterial lysate, or Sf9 cytosol was preincubated with the immunopellets in a final volume of 30 µl on ice for 20 min with suspension of the pellets by shaking the tubes every 3 min. The hydroxylapatite pool was then added and reaction mixtures were brought up to a final volume of 100 ul, and incubations were maintained on ice for 35 min with suspension of the pellets by shaking the tubes every 3 min. At the end of the incubation, the pellets were washed three times with 1 ml of HEG buffer (10 mm Hepes, pH 7.4, 1 mm EDTA, 10% glycerol), and proteins were resolved by SDS-PAGE and Western blotting.

Expression of p60 and GST-FKBP52 Fusion Protein—Bacterially expressed p60/Hop was prepared as described previously (35). For bacterial lysates containing GST-FKBP52, the expression plasmid containing the cDNA for the 59-kDa rabbit immunophilin subcloned into the Smal site of pGEX-2T prepared by Le Bihan, et al. (37) was used to transform E. coli strain BL21(DE3). Purification of rabbit FKBP52 was performed by binding the GST-FKBP52 to GSH-agarose and incubation at 4 °C with thrombin, which cleaves at a site between the GST domain and the FKBP52 domain.

Production of the Fusion Protein GST-Raf (COOH Terminus)—For bacterial expression of GST-Raf (COOH terminus), an in-frame deletion of amino acids 26–309 of human c-Raf-1 following digestion with PvuII and BgII (41), was subcloned into the pGEX-2T bacterial expression vector and in-frame with the GST propeptide to generate pGEXANRaf. The resulting construct was transformed into E. coli BL21(DE3). A control construct including GST in fusion with the first 25 amino acids of human c-Raf-1 behaved similarly as GST alone, in that it bound neither to p50cdc37 nor to hsp90 (data not shown).

Binding of Purified FLAG-p50cdc37 to Raf and GST-Raf (COOH Terminus)

minus)-Control E. coli and bacteria expressing the GST-tagged Raf (COOH terminus) were sonicated in phosphate-buffered saline, and 50 μl of lysate were immobilized on 15 μl of glutathione-cross-linked agarose. v-Raf was immunoabsorbed from 3Y1 cytosol (200 µl) by rotation with the C-12 rabbit anti-Raf-1 IgG prebound to 8 μl of protein A-Sepharose. The immune pellets were washed two times with 1 ml of TEG plus 0.1% Triton X-100, then two times with TEG (for native Raf heterocomplexes, 20 mm molybdate was present in the wash buffers). The pellets were then suspended in TEG buffer containing 0.5 m NaCl and stripped of Raf-associated hsp90 by heating for 1 h at 30 °C followed by two buffer washes prior to incubation with 30 μ l of cytosol from Sf9 cells expressing FLAG-p50^{cdc37}, 40 μ l of purified FLAGp50cdc37, or 45 μl of purified bacterially expressed rabbit FKBP52. Incubations were on ice for 35 min with suspension of the pellets by shaking the tubes every 3 min. At the end of the incubation, the pellets were washed three times with 1 ml of HEG, and proteins were resolved by SDS-PAGE and Western blotting.

Preparation of a Recombinant Baculovirus Expressing FLAG-tagged p50°dc37"—The cDNA for p50°cdc37, isolated from a human lymphocyte cDNA library through hybridization with the previously described chick cdc37 cDNA homolog (5, 10), served as template to amplify by polymerase chain reaction the open reading frame, starting from codon 2 and including 285 base pairs of 3'-untranslated sequence. The amplified human p50°dc37 cDNA was subcloned into the NotI site of pFastBAC1-FLAG, a modified version³ of the baculoviral pFastBAC1 vector (Life Technologies, Inc.), in frame with a FLAG propeptide sequence. The resulting construct was verified by DNA sequencing and subsequently used to generate FLAG-p50°dc37 encoding recombinant baculoviruses and high titer stocks, using the BAC-TO-BAC baculovirus expression system from Life Technologies, Inc.)

³ N. Grammatikakis, unpublished results.

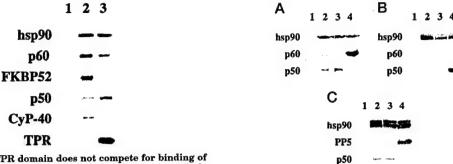


Fig. 1. The PP5 TPR domain does not compete for binding of p50^{cdc37} to hsp90. Protein A-Sepharose pellets linked to 3G3 antibody alone or 3G3 prebound with purified hsp90 were incubated on ice with 30 μl of the rabbit brain hydroxylapatite pool containing p60/Hop, FKBP52, p50^{cdc37} and CyP-40 (but not hsp90) in the presence or absence of 30 μg of purified FLAG-tagged TPR domain of PP5. After washing, pellet-associated proteins were resolved by SDS-PAGE and Western blotting. Lane 1, 3G3 pellet without hsp90 incubated with hydroxylapatite pool; lane 2, 3G3 pellet with bound hsp90 incubated with hydroxylapatite pool; 3G3 pellet with bound hsp90 incubated with hydroxylapatite pool and purified PP5 TPR.

Purification of FLAG-p50°-dc37 from Sf9 Cells—Sf9 cells (1.8×10^{7}) were cultured into T-162 cm tissue culture flasks and infected with a baculovirus expressing FLAG-p50°-dc37 at a multiplicity of infection of 3, then incubated for 2 days at 27 °C. Cytosol was prepared from infected cells and diluted 1:1 with TEG, the nonionic detergent Nonidet P-40 was added to 0.02%, and the diluted cytosol was rotated for 1 h at 4 °C and centrifuged at $100,000\times g$. FLAG-tagged p50°-dc37 was then purified using M2-agarose beads (IBI) according to manufacturer's instructions.

Preparation of an Antibody against $p50^{cdc37}$ —Human $p50^{cdc37}$ (amino acids 2–378) expressed as GST fusion protein was purified by GSH-Sepharose chromatography and used to generate $p50^{cdc37}$ -specific antisera in rabbits. Although the rabbit anti- $p50^{cdc37}$ antiserum exhibits a wide reactivity for $p50^{cdc37}$ across species, it does not recognize the endogenous $p50^{cdc37}$ expressed in insect Sf9 host cells.

RESULTS

Competition for Binding of p50cdc37 to hsp90-In a previous study (29), we showed that a fragment containing the TPR domains of CyP-40 competed for the binding of FKBP52 and CyP-40 to hsp90. However, the binding of p60/Hop and p 50^{cdc37} was not inhibited by the highest achievable level of the CyP-40 TPR fragment. Subsequently, we found that the fragment of PP5 containing its four TPRs bound much more tightly to hsp90 and competed for p60/Hop binding (28). In Fig. 1, we use this tight binding PP5 TPR fragment to compete for the binding of p50cdc37 and several TPR domain proteins to hsp90. In this experiment, an immune pellet alone (lane 1) or immune pellets prebound with purified hsp90 (lanes 2 and 3) were incubated with an hsp90-free hydroxylapatite pool of rabbit brain cytosol (29) that contains p50cdc37 as well as p60/Hop, FKBP52, and CyP-40. As shown in lane 2 (Fig. 1), all four of these proteins bound to hsp90. However, in the presence of the PP5 TPR fragment (lane 3) binding of CyP-40 and FKBP52 was blocked and p60/Hop binding was inhibited. The p60/Hop band was probed with 125 I-labeled counter antibody, excised, and counted to determine the extent of inhibition. The PP5 TPR domain fragment (lane 3) reduced the binding of p60/Hop by 65% but it did not compete for the binding of p50cdc37 to hsp90 (cf. lanes 2 and 3).

In contrast to the TPR domain fragment, intact TPR domain proteins do compete for binding of p50^{cdc37} to hsp90. In the experiment of Fig. 2A, hsp90-bound 3G3 immune pellets were preincubated with buffer (lane 2), with lysate from control bacteria (lane 3), or with lysate from bacteria expressing p60/Hop (lane 4). The pellets were then incubated with the rabbit brain hydroxylapatite pool, and binding of p50^{cdc37} to hsp90

Fig. 2. p50^{cdc37} and TPR proteins compete for the binding of each other to hsp90. A, bacterially expressed p60/Hop competes for binding of p50^{cdc37} to hsp90. Pellets with 3G3 antibody alone or 3G3 prebound with hsp90 were preincubated on ice in the presence of lysate from control bacteria or bacteria expressing p60/Hop, then incubated with the rabbit brain hydroxylapatite pool. Lane 1, pellet without hsp90; lane 2, hsp90-bound pellet; lane 3, hsp90-bound pellet preincubated with control bacterial lysate; lane 4, hsp90-bound pellet preincubated with lysate from bacteria expressing p60/Hop. B, Sf9-expressed p50^{cdc37} competes for binding of p60/Hop to hsp90. Pellets were preincubated in the presence of lysate from Sf9 cells transfected with wild-type baculovirus or Sf9 cells expressing FLAG-p50^{cdc37}, then incubated with the rabbit brain hydroxylapatite pool. p50^{cdc37} was detected with enti-FLAG antibody. Lane 1, pellet without hsp90; lane 2, hsp90-bound pellet; lane 3, hsp90-bound pellet plus control Sf9 lysate; lane 4, hsp90-bound pellet plus lysate from Sf9 cells expressing p50^{cdc37}. C, Sf9-expressed PP5 competes for binding of p50^{cdc37} to hsp90. Pellets were treated as in B. Lane 1, pellet without hsp90; lane 2, hsp90-bound pellet; lane 3, hsp90-bound pellet plus control Sf9 lysate; lane 4, hsp90-bound pellet plus lysate from Sf9 cells expressing Pp5.

was assayed. It is clear from lane 4 that p60/Hop competes for the binding of p50 $^{cdc^{37}}$ to hsp90. In Fig. 2B, hsp90-bound immune pellets were preincubated with lysate from Sf9 cells expressing FLAG-p50 $^{cdc^{37}}$ and then incubated with the hydroxylapatite pool. In the presence of the Sf9-expressed p50 $^{cdc^{37}}$ (lane 4), the binding of p60/Hop to hsp90 was competed. As shown in Fig. 2C, Sf9-expressed FLAG-PP5 also competes for the binding of p50 $^{cdc^{37}}$ to hsp90.

The cloning and sequencing of p50^{cdc37} showed that it does not possess a TPR domain (6, 7),² yet intact TPR domain proteins compete for its binding to hsp90. As shown in the experiment of Fig. 1, we have occasionally observed an increase in the amount of p50^{cdc37} binding to hsp90 when the PP5 TPR fragment is present. Such an increase in p50^{cdc37} binding would occur if binding of TPR proteins to the TPR acceptor site on hsp90 prevented access of p50^{cdc37} to its binding site, but the small PP5 TPR fragment did not.

p50cdc37 Does Not Exist in Native hsp90 Heterocomplexes with TPR Proteins-These competition data suggest that the binding site for p50cdc37 may be close enough to the TPR binding site on the surface of hsp90 such that the binding of a protein to one site blocks access of the other protein to its binding site. If that is true, p50cdc37 should not exist in a native hsp90-TPR protein complex unless there is a binding site for each of the proteins on each half of the hsp90 dimer. In which case, immunoadsorption of an hsp90-bound TPR protein should yield not only co-immunoadsorption of some $p50^{cdc37}$ but also of other TPR proteins. In the experiment of Fig. 3, either hsp90 or p60/Hop was immunoadsorbed from rabbit reticulocyte lysate and the washed immune pellets were assayed for coadsorbed proteins. Immunoadsorption of hsp90 (lane 2) yielded coadsorption of the four TPR proteins (p60/Hop, PP5, FKBP52, and CyP-40) as well as the non-TPR-containing p50cdc37. Immunoadsorption of p60/Hop (lane 4) yielded coadsorption of a substantial amount of hsp90 but no coadsorption of p50cdc37 or of other TPR proteins.

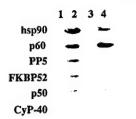


Fig. 3. Native hsp90 p60/Hop heterocomplexes do not contain p50°de37. Aliquots (150 µl) of rabbit reticulocyte lysate were immuno-adsorbed with the 3G3 antibody against hsp90 or the F5 antibody against p60/Hop. Lane 1, nonimmune IgM; lane 2, 3G3 anti-hsp90; lane 3, nonimmune IgG; lane 4, F5 anti-p60/Hop.

It is possible that p60/Hop is unique among TPR proteins in that it is present in hsp90 heterocomplexes free of $p50^{cdc37}$. We were unable to test this possibility by coimmunoadsorption of hsp90 heterocomplexes with antibodies directed against p50cdc37 or the immunophilins because of their substantial cross-reactivity. The antiserum against p50 cdc37 (α -p50), for example, reacts on immunoblots with both PP5 and CyP-40 (data not shown). Given the cross-reactivity of the antisera, we used a monoclonal antibody against the FLAG epitope to immunoadsorb Sf9-expressed FLAG-p50cdc37 and FLAG-PP5 and assayed for coimmunoadsorbed proteins. In the experiments of Fig. 4, a small amount of Sf9 cytosol with the expressed FLAGtagged protein was first incubated with rabbit reticulocyte lysate to ensure complete equilibration of the FLAG-p50cde and FLAG-PP5 with rabbit hsp90. The FLAG-tagged proteins were then immunoadsorbed with the M2 monoclonal anti-FLAG IgG, and coadsorbed proteins were assayed. It is clear that immunoadsorption of FLAG-p50cdc37 yields coadsorption of hsp90, but there is no coadsorption of the rabbit TPR domain proteins PP5 or FKBP52. Similarly, immunoadsorption of FLAG-PP5 yielded coadsorption of hsp90, but there is no coadsorption of p50cdc37. Taken together, these coimmunoadsorption observations and the competition data of the previous section lead us to conclude that p50cdc37 can bind to hsp90 when the TPR acceptor site is occupied by the TPR domain fragment of PP5 but not when the site is occupied by an intact TPR domain protein.

p50^{cdc37} Binds Directly to Raf—The exclusive binding of a TPR domain protein or p50^{cdc37} to hsp90 explains why there are separate heterocomplexes but not why the dominant Rafhsp90 heterocomplex contains p50^{cdc37} instead of an immunophilin. The experiments of Fig. 5 were performed to determine if p50^{cdc37} also binds directly to Raf. In the experiment of Fig. 5A, v-Raf-1 was immunoadsorbed from rat 3Y1 cell cytosol, and the native heterocomplex of Raf with rat hsp90 and p50^{cdc37} is shown in lane 2. Raf was stripped of its associated proteins (lane 4) and the stripped Raf immune pellet was incubated with purified FLAG-p50^{cdc37} (lane 6). As shown in lanes 5 and 6 of Fig. 5A, FLAG-p50^{cdc37} binds to the immune pellet in a manner that is specific for the presence of v-Raf-1.

Fig. 5B shows that the catalytic domain of bacterially derived c-Raf is sufficient for direct p50^{cdc37} binding. In this experiment the GST-tagged c-Raf COOH-terminal fragment expressed in E. coli was immobilized on glutathione-agarose and stripped with salt and heating (lane 2). When the immobilized c-Raf catalytic domain was incubated with cytosol from Sf9 cells expressing FLAG-p50^{cdc37}, Raf-p50^{cdc37} complexes were formed (Fig. 5B, lane 4). The immobilized c-Raf catalytic domain fragment also bound purified FLAG-p50^{cdc37} (lane 6) but not purified FKBP52 (lane 8).

It is known that the catalytic domain of c-Raf is sufficient for forming the heterocomplex with hsp90 (31), and these data of Fig. 5 suggest a model in which p50^{cdc37} may contact Raf as

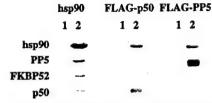


Fig. 4. p50^{cdc37}, PP5 and FKBP52 exist in independent heterocomplexes with hsp90. Aliquots (100 μl) of rabbit reticulocyte lysate were immunoadsorbed with nonimmune IgM or 3G3 antibody against hsp90. Other 100-μl aliquots of reticulocyte lysate were incubated for 30 min at 30 °C with 10 μl of 5f9 cytosol overexpressing FLAG-p50^{cdc37} or FLAG-PP5, and then immunoadsorbed with nonimmune IgG or the M2 monoclonal IgG against the FLAG epitope. Lane 1, immunoadsorption with nonimmune antibody, lane 2, immunoadsorption with the antibody indicated at the top of each pair of lanes. Note that the AC88 antibody used to blot hsp90 reacts with rabbit but not insect (Sf9) hsp90 (31). Because PP5 migrates close to FKBP52 on SDS-PAGE, any FKBP52 that might be present in the immune adsorbate would be obscured by the large amount of FLAG-PP5; thus, FKBP52 was not assayed.

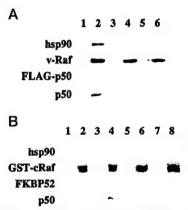


FIG. 5. **p50**^{cdc37} binds directly to Raf. A, p50^{cdc37} binds directly to v-Raf. Immunoadsorbed v-Raf was stripped of Raf-associated proteins, and two of these stripped samples were incubated with purified FLAG-p50^{cdc37} as described under "Methods." Lane 1, adsorption with nonimune rabbit IgG; lane 2, native Raf heterocomplex adsorbed with C-12 anti-Raf-1; lane 3, stripped nonimmune pellet; lane 4, stripped immune pellet; lane 6, stripped nonimmune pellet incubated with purified FLAG-p50^{cdc37}, lane 6, stripped immune pellet incubated with purified FLAG-p50^{cdc37}, lane 6, stripped immune pellet incubated with purified FLAG-p50^{cdc37}, lane 6, stripped immune pellet incubated with purified FLAG-p50^{cdc37}, lane 6 (SST tagged Raf COOH-terminal fragment was stripped of associated proteins and incubated as described. Lane 1, GST; lane 2, GST-Raf COOH terminus; lanes 3 and 4, immobilized GST (lane 3) or GST-Raf COOH terminus (lane 4) incubated with lysate from Sf9 cells expressing FLAG-p50^{cdc37}; lanes 5 and 6, GST or GST-Raf COOH terminus incubated with purified FLAG-p50^{cdc37}; lanes 7 and 8, GST or GST-Raf COOH terminus incubated with purified FKBP52.

well as hsp90 when it is in the Rafhsp90·p50^{cdc37} heterocomplex. The direct binding of p50^{cdc37} to Raf could allow the kinase to determine its existence in hsp90 heterocomplexes containing p50^{cdc37} as opposed to immunophilins.

DISCUSSION

Previous studies have shown that FKBP52 and CyP-40 compete with each other for binding to hsp90 (21, 24) and that these two immunophilins and the TPR-containing protein phosphatase, PP5, exist in separate heterocomplexes with hsp90 (28). In this work, we provide evidence that p50^{cdc37} cannot bind to hsp90 when the TPR acceptor site on hsp90 is occupied by one of the TPR domain proteins, such as p60/Hop or PP5. However, p50^{cdc37} does bind to hsp90 when the small TPR domain fragment of PP5 occupies the TPR acceptor site and prevents binding of the TPR domain proteins. These com-

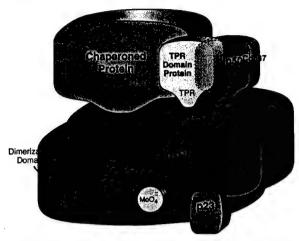


Fig. 6. Model of protein binding sites on hsp90. The chaperoned protein represents any of the many protein kinases or transcription factors that are recovered from cytosols in stable complexes with hsp90. The TPR protein can be p60/Hop, PP5, or any of the immunophilins that have been identified in transcription factor hsp90 heterocomplexes. To date, p50°dc37 has been recovered only with protein kinase has 90° heterocomplexes. date, polybdate (MoO_4^-) , which stabilizes hsp90 in its ATP-dependent conformation (50), interacts with the nucleotide binding site.

petition data suggest that the p50cdc37 binds to a site on the surface of hsp90 that is close to the TPR binding site and that binding of a protein to one site may block binding of a protein to the other site.

It could be argued that binding of a protein, such as p60/Hop, PP5, or an immunophilin, to the TPR binding site on hsp90 influenced the conformation of hsp90 such that the affinity of a p50cdc37 binding site located at some distance from the TPR binding site was reduced. However, the fact that binding of the PP5 TPR fragment to hsp90, if not augmenting, at least does not reduce the binding of p50cdc37 argues against such an allosteric effect. Thus, we propose that $p50^{cdc37}$ binds to a site on hsp90 that is topologically adjacent to the TPR binding site, and at any instant in time, an hsp90 heterocomplex contains either p50cdc37 or one of the TPR domain proteins.

Although hsp90 is present in cytosols as a dimer, it is likely that only one molecule of p50cdc37 or TPR domain protein can be bound by the dimer. In the event that independent binding sites were available on each dimer, we should have recovered mixed complexes in which immunoadsorption of one TPR protein from cytosol yields coimmunoadsorption of other TPR proteins and p50cdc37. A stoichiometry in which one of these proteins is bound per hsp90 dimer is consistent with careful crosslinking studies of Gehring and his co-workers (42-44), who established a stoichiometry for untransformed steroid receptor heterocomplexes of one steroid-binding protein, two molecules of hsp90, and one molecule of immunophilin. However, it must be emphasized that the stoichiometry of hsp90 immunophilin and hsp90-p50cdc37 complexes has not been determined directly in the absence of receptors or protein kinases, and the stoichiometry in two-protein versus the three-protein complexes could be different.

hsp90 has been found in complex with a confusing variety of proteins, and the model shown in Fig. 6 is presented to sort out established binding domains on the surface of hsp90. More than a dozen transcription factors and more than a dozen protein kinases have been reported to be in heterocomplex with hsp90 (see Table I in Ref. 1 for summary). These proteins are represented by the chaperoned protein in Fig. 6, and they must bind to a common domain (chaperoning domain) on hsp90 which appears to be located in its COOH-terminal half (45, 46). Under nondenaturing conditions, hsp90 purifies as a dimer, with the dimerization site likely lying in a COOH-terminal region (47). The NH2-terminal domain (amino acids 1-221) of hsp90 contains a nucleotide binding site (48, 49). Binding of p23 to the ATP-dependent conformation of hsp90 requires regions outside of the 1-221 domain, but on the basis of the observations of Toft and his co-workers (49, 50), it is reasonable to predict that, in the three-dimensional structure of hsp90, the nucleotide binding domain (ATP/ADP switch domain), the p23 binding site, and the chaperoning domain are situated close to each other, forming an active center that determines a conformational change in the chaperoned protein.

The TPR binding domain of hsp90 is required for the binding p60/Hop (34), which in turn is required for steroid receptor hsp90 heterocomplex assembly (35) and dissociates from hsp90 during the assembly process (51). Mature steroid receptor heterocomplexes have been reported to contain FKBP51, FKBP52, CyP-40, or PP5 bound to this TPR binding site (1, 2). Only one of these TPR proteins exists in a receptor hsp90 heterocomplex at any time (24, 25). However, because binding of TPR proteins to the TPR binding site on hsp90 is a reversible process, over time, a single receptor hsp90 heterocomplex may be associated with PP5 and any of the TPR domain immunophilins. A 38-kDa FKBP homolog with three TPR domains called ARA3 has been isolated with dioxin (Ah) receptor-hsp90 complexes (52). In addition to binding to hsp90, ARA3 appears to bind to the dioxin receptor directly (52), and there is indirect evidence that FKBP52 may contact the transformed glucocorticoid receptor (53). Thus, in Fig. 6, the TPR binding site on hsp90 has been placed such that the TPR protein that occupies the site may also contact the chaperoned protein.

The evidence of this study suggests that the p50^{cdc37} component of protein kinase hsp90 heterocomplexes binds, in vitro, to a site that is topologically adjacent to the TPR binding site on hsp90 but that $p50^{cdc^{37}}$ and a TPR domain protein may not be able to bind to the same hsp90 dimer. The dashed borders of the TPR domain protein and p50cdc37 in Fig. 6 indicate the overlapping space occupied by both proteins that accounts for their mutual competition for binding to hsp90. Because p50cdc37 binds directly to Raf (Fig. 5) and to Cdk4 (6, 10), it has also been positioned such that it could contact the chaperoned protein as well as hsp90.

In the dynamic state when Raf-hsp90 complexes are being assembled, dissociation of the p60/Hop component of the assembly machinery would expose on hsp90 both the binding site for TPR domains and the adjacent binding site for p50cdc37. As both the TPR domain proteins and p50cdc37 bind in a readily reversible manner to their respective sites on hsp90, simultaneous binding of p50cdc37 directly to Raf should rapidly select for Raf·hsp90·p50^{cdc37} complexes, which is the composition of native Raf-hsp90 heterocomplexes isolated from cytosols (31). Thus, the combination of exclusive binding of p 50^{cdc37} versus a TPR domain protein to hsp90 plus direct binding of $p50^{cdc37}$ to Raf allow the protein kinase to determine the dominant heterocomplex composition.

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REFERENCES

- 1. Pratt, W. B., and Toft, D. O. (1997) Endocr. Rev. 18, 306-360

- Fratt, W. B., and 10ft, D. O. (1997) Endocr. Rev. 18, 306-350
 Pratt, W. B. (1997) Annu. Rev. Pharmacol. Toxicol. 37, 297-326
 Brugge, J. S. (1986) Curr. Top. Microbiol. Immunol. 123, 1-22
 Hunter, T., and Poon, R. Y. C. (1997) Trends Cell Biol. 7, 157-161
 Grammatikakis, N., Grammatikakis, A., Yoneda, M., Yu, Q., Banerjee, S. D., and Toole, B. P. (1995) J. Biol. Chem. 270, 16198-16205
 Stepneng, L. Lorg, Y. Parker, S. P. and Harmar, J. W. (1906) Conv. Page 146.
- 6. Stepanova, L., Leng, X., Parker, S. B., and Harper, J. W. (1996) Genes Dev. 10,

1491-1502

1491–1502
7. Perdew, G. H., Wiegand, H., Vanden Heuvel, J. P., Mitchell, C., and Singh, S. S. (1997) Biochemistry 36, 3600–3607
8. Dey, B., Lightbody, J. J., and Bochelli, F. (1996) Mol. Biol. Cell 7, 1405–1417
9. Cutforth, T., and Rubin, G. M. (1994) Cell 77, 1027–1036

- Cutforth, T., and Rubin, G. M. (1994) Cell 77, 1027-1036
 Grammatikakis, N., Grammatikakis, A., Piwinica-Worms, H., Toole, B. P., and Cochran, B. H. (1996) Meeting on the Cell Cycle. Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, p. 72 (abstr.)
 Yem, A. W., Tomasselli, A. G., Heinrikson, R. L., Zurcher-Neely, H., Ruff, V. A., Johnson, R. A., and Deibel, M. R., Jr. (1992) J. Biol. Chem. 267, 2868-2871
 Lebeau, M.-C., Massol, N., Herrick, J., Faber, L. E., Renoir, J.-M., Radanyi, C., and Baulieu, E.-E. (1992) J. Biol. Chem. 267, 4281-4284
 Tai, P. K. Albers, M. W. Chang, H., Faber, L. E., and Schreiber, S. L. (1992)

- 13. Tai, P. K., Albers, M. W., Chang, H., Faber, L. E., and Schreiber, S. L. (1992)
- Science 256, 1315-1318

 14. Peattie, D. A., Harding, M. W., Fleming, M. A., De Cenzo, M. T., Lippke, J. A., Livingston, D. J., and Benasutti, M. (1992) Proc. Natl. Acad. Sci. U. S. A. 89, 10974-10978
- 15. Smith, D. F., Baggenstoss, B. A., Marion, T. N., and Rimerman, R. A. (1993)
- J. Biol. Chem. 268, 18365–18371 16. Smith, D. F., Albers, M. W., Schreiber, S. L., Leach, K. L., and Deibel, M. R.,

- Smith, D. F., Albers, M. W., Schreiber, S. L., Leach, K. L., and Deibel, M. R., Jr. (1993) J. Biol. Chem. 268, 24270-24273
 Nair, S. C., Rimerman, R. A. Toran, E. J., Chen, S., Prapapanich, V., Butts, R. N., and Smith, D. F. (1997) Mol. Cell. Biol. 17, 594-603
 Ratajczak, T., Carrello, A., Mark, P. J., Warner, B. J., Simpson, R. J., Moritz, R. L., and House, A. K. (1993) J. Biol. Chem. 268, 13187-13192
 Kieffer, L. J., Seng, T. W., Li, W., Osterman, D. C., Handschumacher, R. E., and Bayney, R. M. (1993) J. Biol. Chem. 268, 12303-12310
 Sikorski, R. S., Boguski, M. S., Goebl, M., and Hieter, P. (1990) Cell 60, 207, 217 307-317
- 21. Ratajczak, T., and Carrello, A. (1996) J. Biol. Chem. 271, 2961-2965
- Radanyi, C., Chambraud, B., and Baulieu, E. E. (1994) Proc. Natl. Acad. Sci. U. S. A. 91, 11197–11201
- 23. Hoffmann, K., and Handschumacher, R. E. (1995) Biochem. J. 307, 5-8
- Owens-Grillo, J. K., Hoffmann, K., Hutchison, K. A., Yem, A. W., Deibel, M. R., Handschumacher, R. E., and Pratt, W. B. (1995) J. Biol. Chem. 270, 20479-20484
- Renoir, J. M., Mercier-Bodard, C., Hoffman, K., Le Bihan, S., Ning, Y. M., Sanchez, E. R., Handschumacher, R. E., and Baulieu, E. E. (1995) Proc. Natl. Acad. Sci. U. S. A. 92, 4977-4981
- 26. Chen, M.S., Silverstein, A. M., Pratt, W. B., and Chinkers, M. (1996) J. Biol.
- Chen, M.-S., Silversteil, A. M., Flatt, W. B., and Ominters, M. (1994) Proc. Natl. Acad. Sci. U. S. A. 91, 11075-11079
 Silverstein, A. M., Galigniana, M. D., Chen, M.-S., Owens-Grillo, J. K., Chinkers, M., and Pratt, W. B. (1997) J. Biol. Chem. 272, 16224-16230
 Owens-Grillo, J. K., Czar, M. J., Hutchison, K. A., Hoffmann, K., Perdew, G. H., and Pratt, W. B. (1996) J. Biol. Chem. 271, 13468-13475

- 30. Whitelaw, M. L., Hutchison, K., and Perdew, G. H. (1991) J. Biol. Chem. 266, 16436-16440

- Stancato, L. F., Chow, Y-H., Hutchison, K. A., Perdew, G. H., Jove, R., and Pratt, W. B. (1993) J. Biol. Chem. 268, 21711-21716
 Stancato, L. F., Chow, Y-H., Owens-Grillo, J. K., Yem, A. W., Deibel, M. R., Jove, R., and Pratt, W. B. (1994) J. Biol. Chem. 269, 22157-22161
 Stancato, L. F., Silverstein, A. M., Owens-Grillo, J. K., Chow, Y-H., Jove, R., and Pratt, W. B. (1997) J. Biol. Chem. 272, 4013-4040
- 34. Chen, S., Prapanich, V., Rimerman, R. A., Honoré, B., and Smith, D. F. (1996)

 Mol. Endocrinol. 10, 682-693
- Mol. Endocrinol. 10, 682-683
 Dittmar, K. D., Hutchison, K. A., Owens-Grillo, J. K., and Pratt, W. B. (1996)

 J. Biol. Chem. 271, 12833-12839

 Smith, D. F., Sullivan, W. P., Marion, T. N., Zaitsu, K., Madden, B., McCormick, D. J., and Toft, D. O. (1993) Mol. Cell. Biol. 13, 869-876
 Le Bihan, S., Renoir, J. M., Radanyi, C., Chambraud, B., Joulin, V., Catelli, R. (2002) Explanation, Physics B. (2002) Explanation (2004) Explanation (2004) Explanation (2004) Explanation (2004)
- M. G., and Baulieu, E. E. (1993) Biochem. Biophys. Res. Commun. 195, 600-607
- 38. Ruff, V. A., Yem, A. W., Munns, P. L., Adams, L. D., Reardon, I. M., Deibel, M. R., and Leach, K. L. (1992) J. Biol. Chem. 267, 21285-21288
- 39. Erhart, J. C., Duthu, A., Ullrich, S., Appella, E., and May, P. (1988) Oncogene 3. 595-603
- 40. Hutchison, K. A., Dittmar, K. D., Czar, M. J., and Pratt, W. B. (1994) J. Biol. Chem. 269, 5043-5049
 Bruder, J. T., Heidecker, G., and Rapp, U. R. (1992) Genes Dev. 6, 545-556
- Rexin, M., Busch, W., and Gehring U. (1991) J. Biol. Chem. 266, 24601–24605
 Rehberger, P., Rexin, M., and Gehring, U. (1992) Proc. Natl. Acad. Sci. U. S. A. 89, 8001–8005
- 44. Segnitz, B., and Gehring, U. (1995) Proc. Natl. Acad. Sci. U. S. A. 92, 2179-2183
- 45. Shaknovich, R., Schue, G., and Kohtz, D. S. (1992) Mol. Cell. Biol. 12,
- Sullivan, W. P., and Toft, D. O. (1993) J. Biol. Chem. 268, 20373–20379
 Minami, Y., Kimura, Y., Kawasaki, H., Suzuki, K., and Yahara, I. (1994) Mol. Cell. Biol. 14, 1459-1464
- 48. Prodromou, C., Roe, S. M., O'Brien, R., Ladbury, J. E., Piper, P. W., and Pearl,
- Prodromou, C., Roe, S. M., O'Brien, R., Ladbury, J. E., Piper, P. W., and Pearl, L. H. (1997) Cell 90, 65-75
 Grenert, J. P., Sullivan, W. P., Fadden, P., Haystead, T. A. J., Clark, J., Mimnaugh, E., Krutzch, H., Ochel, H.J., Schulte, T. W., Sausville, E., Neckers, L. M., and Toft, D. O. (1997) J. Biol. Chem. 272, 23843-23850
 Sullivan, W., Stensgard, B., Caucutt, G., Bartha, B., McMahon, N., Alnemri, E. S., Litwack, G., and Toft, D. O. (1997) J. Biol. Chem. 272, 8007-8012
 Smith, D. (1993) Mol. Endocrinol. 7, 1418-1429
 Carver, L. A., and Bradfield, C. A. (1997) J. Biol. Chem. 272, 11452-11456
 Carver, L. A., and Bradfield, C. A. (1997) J. Biol. Chem. 272, 11452-11456

- 53. Czar, M. J., Lyons, R. H., Welsh, M. J., Renoir, J. M., and Pratt, W. B. (1995)
- Mol. Endocrinol. 9, 1549-1560

400	Gene Name	ZR75	YY3	YY1	468	MPI	231 (log base 2 ratio
W06980	•	0.303 0.194	0.063	0.302 0.212	1.535 -0.090	0.171 0.800	1.275 Induction relative to 76n 1.112 cell line)
	(2'-5') oligoadenylate synthetase E 14-3-3 PROTEIN TAU	0.176	0.334	0.036	0.127	0.803	0.554
AA775223	15-HYDROXYPROSTAGLANDIN DEHYDROGENASE	-0.028 -0.319	-0.055 -0.151	-0.080 -0.134	0.591 -1.089	-0.262 -0.508	0.869 0.584
AA464970 AA846573	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3	-0.498	0.075	-0.408	-0.611	-0.326	0.961
AA678065	2,3-bisphosphoglycerate mutase	-0.210 -0.543	-0.244 -0.077	-0.191 0.024	-0.285 0.255	-0.259 0.400	1.269 0.793
AA088837 AA251770	26S PROTEASE REGULATORY SUBUNIT 4 26S PROTEASE REGULATORY SUBUNIT 7	0.220	0.554	-0.178	1.239	0.740	0.981
AA464557	26S PROTEASOME REGULATORY SUBUNIT P31	0.135 0.906	0.668 0.742	0.335 0.404	0.641 0.144	0.436 0.603	0.810 0.894
AA779417 T80846	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 3-HYDROXYANTHRANILATE 3,4-DIOXYGENASE	0.620	1.535	1.007	-0.098	0.885	1.137
AA458779	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	-1.046 -0.623	-0.400 -0.390	-0.440 -0.469	-0.224 -0.927	-0.823 -1.019	0.536 0.652
	40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 40S RIBOSOMAL PROTEIN S15A	2.261	0.241	0.835	1.562	2.252	0.798
	40S RIBOSOMAL PROTEIN S23 40S RIBOSOMAL PROTEIN S27	0.105 -0.513	0.044 -0.220	0.394 0.376	-0.191 0.378	0.593 -0.173	0.644 1.114
AA683050	40S RIBOSOMAL PROTEIN S8	-0.009	0.013	0.166	-0.003 0.385	0.966 0.726	1.107 1.036
	4-hydroxyphenylpyruvate dioxygenase 5' nucleotidase (CD73)	0.414 -0.030	0.245 0.349	0.331 -0.043	-0.328	0.062	0.936
R60343	5' nucleotidase (CD73)	-0.253 0.460	-0.123 0.372	0.053 0.242	0.053 -0.018	0.207 0.280	0.879 0.931
	5,6-DIHYDROXYINDÓLE-2-CARBOXYLIC ACID OXIDASE PRECURSOR 5-HT2AR	-1.358	-1.233	-1.011	-1.345	-1.475	0.710
N47111	5-hydroxytryptamine (serotonin) receptor 2C	0.248 1.441	0.763 1.174	-0.138 0.632	0.022 0.816	0.203 1.214	0.516 0.450
AA703169 N36174	5-hydroxytryptamine (serotonin) receptor 3 5-HYDROXYTRYPTAMINE 2B RECEPTOR	0.256	0.119	0.464	-0.203	0.472	0.876
T49652	5-LIPOXYGENASE ACTIVATING PROTEIN	0.294 0.447	0.255 0.082	-0.048 0.754	0.284 0.496	-0.084 0.071	1.557 2.293
AA459104	5-methyltetrahydrofolate-homocysteine methyltransferase 60S RIBOSOMAL PROTEIN L13	-0.495	-0.350	-0.355	-0.224	-0.129	1.370
AA775874	60S RIBOSOMAL PROTEIN L18	0.232 1.069	0.345 0.545	0.535 1.014	0.447 0.174	0.472 1.123	1.318 0.648
	60S RIBOSOMAL PROTEIN L24 60S RIBOSOMAL PROTEIN L30	0.392	-0.118	0.468	0.011	0.706	0.632
	60S RIBOSOMAL PROTEIN L34	0.384 0.562	0.422	0.265 0.668	0.492 0.484	0.631 0.920	0.537 0.391
AA441933	60S RIBOSOMAL PROTEIN L38 64 KD AUTOANTIGEN D1	-0.336	0.117	0.123	0.452	0.133	0.458 0.647
	65 KD YES-ASSOCIATED PROTEIN 69 KD ISLET CELL AUTOANTIGEN	0.010 0.085	0.208 0.270	0.310 0.223	0.550 -0.415	0.681 0.117	0.573
AAR77347	6-PYRIJVOYI TETRAHYDROBIOPTERIN SYNTHASE	-0.288	0.211	0.157	-0.155 0.079	0.344 0.276	1.070 0.929
AA459909 N63940	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) ACETYLCHOLINESTERASE PRECURSOR	0.249 0.132	0.167 -0.063	0.431 -0.028	0.068	0.621	0.794
	Acid alpha-glucosidase	1.122	0.404	0.500 0.202	0.390 -0.161	0.895 0.635	1.266 0.568
AA490855 W45148	Acid finger protein ZNF173 Acid phosphatase 1, soluble	0.548 0.627	0.460	0.586	0.192	0.906	0.572
T48864	Acid phosphatase 2, lysosomal	0.559 0.669	0.344	-0.120 0.097	0.019 0.271	-0.110 0.607	-0.026 0.304
R08817 W44454	Acid phosphatase type 5 Aconitase 2, mitochondrial	0.295	-0.083	0.027	-0.008	0.118	0.289
AA625888	ACROSIN-TRYPSIN INHIBITOR II PRECURSOR	0.074 -0.201	-0.025 0.007	0.385 0.027	0.038 0.285	0.260 0.042	0.570 0.508
AA732783 AA424824	Acrosomal vesicle protein 1 Actin depolymerizing factor [human, fetal brain, mRNA, 1452 nt]	-0.208	0.106	0.201	0.136	0.154	0.356
AA026609	Actin, alpha 1, skeletal muscle	0.899 0.669	0.470 0.629	0.022 0.379	-0.043 0.405	0.281 0.241	0.868 0.742
	Actin, alpha 2, smooth muscle, aorta Actinin alpha-3	0.558	0.256	0.396	-0.431	-0.054	0.857
R39862	Activated leucocyte cell adhesion molecule Activating transcription factor 3	0.234 0.704	0.458 0.550	0.009 0.428	0.062 0.275	0.209 1.237	0.366 -0.124
H21042 N99003	Active BCR-related gene	0.012	-0.019	-0.259	-0.455 0.317	-0.026 0.784	-0.441 -0.152
AA125981 H95792	Activin A receptor, type II Acyl-coA dehydrogenase	0.162 -0.809	0.398 -0.155	0.218 -0.204	-0.357	-0.730	0.368
AA676663	Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	0.703 -0.147	0.551 -0.179	0.375 -0.436	0.455 -0.505	0.549 0.207	0.718 0.756
N70794 R66006	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain Acyl-Coenzyme A dehydrogenase, long chain	0.232	0.723	0.143	0.042	0.360	0.878
AA464163	Acyl-Coenzyme A dehydrogenase, very long chain	0.487 0.100	0.551 -0.162	0.208 -0.661	0.406 -0.322	0.359 -0.357	1.205 1.223
T65864 W80489	Acyloxyacyl hydrolase (neutrophil) ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYME	-0.066	0.318	-0.240	0.078	-0.194 0.050	1.303 0.658
H41489 N53485	Adaptin, beta 1 (beta prime) Adducin 1 (alpha)	0.067 0.297	0.389 0.887	-0.225 0.226	-0.079 -0.019	0.050	0.179
AA019320	Adducin 2 (beta) {atternative products}	0.241 0.079	0.614 0.593	-0.092 -0.071	0.147 -0.073	0.400 0.548	0.315 0.329
AA461325 AA404486	Adducin 3 (gamma) Adenine nucleotide translocator 2 (fibroblast)	0.534	0.132	-0.150	-0.063	0.232	0.202
AA663439	Adenine nucleotide translocator 3 (liver)	0.277 -0.544	0.270 0.001	0.294 -0.709	0.385 -0.556	0.506 -0.696	0.974 0.370
	Adenomatosis polyposis coli Adenosine A2b receptor	-0.075	0.489	-0.001	-0.251	0.307	0.491
AA683578	ADENOSINE DEAMINASE	-0.588 0.242	-0.311 0.675	-0.040 -0.277	-0.168 -0.250	-0.201 -0.323	0.908 1.067
R12473 R01733	Adenosine kinase Adenosine monophosphate deaminase (isoform E)	0.373	0.477	0.024	-0.049	-0.021	0.991
	Adenosine monophosphate deaminase 1 (isoform M) Adenosine receptor A2	0.087 0.153	-0.277 -0.583	-0.338 0.045	-0.444 -0.471	-0.614 0.294	0.612 0.313
N57553 AA863086	Adenosine receptor A3	-0.006	0.075 0.663	-0.221 0.797	-0.219 0.110	0.189 -0.104	0.656 0.914
AA772803 N45141	Adenylate cyclase activating polypeptide 1 (pituitary) ADENYLATE CYCLASE, TYPE II	0.471 0.504	0.719	0.060	0.366	0.757	0.752
W23690	Adenylate kinase 1	0.296 0.033	0.141 -0.040	0.009 0.052	-0.042 -0.277	0.532 0.350	0.648 0.670
H09730 AA455931	Adenylate kinase 2 (adk2) Adenylosuccinate tyase	0.374	0.628	0.117	0.055	0.091	0.610
AA431414	Adenylosuccinate synthase	-0.305 -0.068	0.149 0.477	0.306 -0.461	0.367 -0.071	-0.004 0.045	0.957 1.126
AA116125 W45572	ADP.ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 ADP-ribosylation factor 1	1.228	1.189	-0.144	0.072	0.393	0.549
AA670422	ADP-ribosylation factor 3	0.120 -0.617	0.189 0.020	0.541 -0.160	-0.203 0.367	-0.461 -0.079	0.637 0.747
T71316 H15085	ADP-ribosylation factor 4 ADP-ribosylation factor 4-like	0.110	0.024	-0.204	-0.178	0.238	0.394
AA629584	ADP-ribosylation factor 5	-0.166 -0.084	0.184 -0.012	-0.329 -0.427	0.027 -0.132	-0.278 0.572	0.207 0.659
N51280	ADP-ribosylation factor 6 ADP-ribosylation factor like 1	-0.373	0.017	0.078	-0.180	-0.148	0.596
AA700172	ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 2 ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	-0.175 0.075	-0.438 0.440	-0.013 0.013	-0.541 0.255	-0.073 0.493	-0.079 0.968
AA701996	ADRENAL SPECIFIC 30 KD PROTEIN	0.456	0.365	0.050	0.129 0.208	0.461	0.555 0.802
R88247 H90431	Adrenergic, beta, receptor kinase 1 Adrenergic, beta-2-, receptor, surface	0.467 0.014	0.694 -0.154	0.211 -0.268	-0.419	-0.147	0.648
AA187349	ADRENODOXIN PRECURSOR	-0.265 -0.112	0.203	-0.182 0.222	0.178 0.327	-0.246 0.110	0.474 0.052
AA446120 W74536	ADRENOMEDULLIN PRECURSOR Advanced glycosylation end product-specific receptor)	0.028	0.498	-0.265	-0.120	0.212	0.653
AA443284	AF-9 PROTEIN	-0.304 2.550	0.081	-0.391 1.184	-0.365 0.556	0.260 1.762	0.271 0.761
N57766 AA025940	Agammaglobulinaemia protein-tyrosine kinase atk AH-receptor	-0.742	-0.304	-0.199	-0.358	-0.166	0.099
N63107	A-KINASE ANCHOR PROTEIN 79 Alanine-qiyoxylate aminotransferase (oxalosis 1; hyperoxaluria I; glycolicaciduria; serine-pyruvate amino	1.402 0.884	0.131 0.850	0.443 0.018	0.043 0.132	0.796 0.319	-0.193 1.054
	Alanyl-tRNA synthetase	1.445	0.480 0.234	1.487 0.070	0.588	0.838 0.126	0.050 -0.356
AA630354	Albumin D-box binding protein	0.333	0.234	0.070	U.VBZ	5.120	J

ACC	Gene Name	ZR75	YY3	YY1	468	MPI	231	(log base 2 ra
	Alcohol dehydrogenase 2 (class I), beta polypeptide	0.637	0.493	-0.753	-0.396	-0.884	0.497	
	Alcohol dehydrogenase 4 (class II), pi polypeptide	0.323	0.808	0.287	0.936	0.259	0.601	
	Alcohol dehydrogenase 5 chi subunit (class III)	0.392	0.847	-0.137	-0.242	-0.036	-0.084	
AA664101	Aldehyde dehydrogenase 1, soluble	0.151	0.704	0.022	0.328	0.243	-0.533	
AA633569	Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)	0.658	0.538	0.587	1.432	0.047	0.310	
	Aldehyde dehydrogenase 6	0.545	0.626	0.877	1.339	0.897	0.712	
N93686	Aldehyde dehydrogenase 7	-0.451	-0.223	-0.267	0.187	0.024	0.669	
R46816	Aldehyde dehydrogenase 7 (NOTE: redefinition of symbol)	0.365	0.412	0.151	-0.123	-0.033	-0.367	
AA443630	Aldehyde dehydrogenase 8	0.794	0.757	0.553	0.140	0.108	1.037	
R93551	ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL X PRECURSOR	0.226	0.518	0.068	0.014	0.743	0.363	
AA775241	Aldolase A	-0.070	-0.234	0.156	0.131	0.051	-0.134	
H72098	Aldolase B, fructose-bisphosphate	0.144	1.280	0.234	-0.074	0.423	0.219	
R39463	Aldolase C, fructose-bisphosphate	0.430	0.516	0.163	0.115	0.230	0.405	
AA190871	Alkaline phosphatase, intestinal	-0.481	-0.108	0.218	-0.354	-0.023	0.288	
AA873885	Alkaline phosphatase, liver/bone/kidney	1.569	1.393	2.053	0.673	1.717	0.836 0.760	
AA150487	Alkaline phosphatase, placental (Regan isozyme)	-0.546	-0.060	-0.231	0.243	-0.149 0.374	0.768	
W69954	Allograft inflammatory factor 1	0.072	-0.037	0.107	-0.368	0.585	0.715	
H95633	ALPHA CRYSTALLIN A CHAIN	-0.105	0.162	0.113	0.106	0.041	-0.117	
AA454175	Alpha mannosidase II isozyme	-0.188	0.494	-0.043	0.495 -0.497	-0.211	0.837	
H23235	ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR	0.387	0.716	0.113		-0.100	0.254	
T98612	Alpha-1 type 3 collagen	0.333	0.397	0.054	-0.162 0.408	1.426	0.149	
AA598507	Alpha-1 type VII collagen	0.818	0.888	0.878 0.072	0.813	1.258	-0.125	
R54968	Alpha-1 type XVI collagen	0.303	0.563	0.264	0.432	1.170	0.320	
R92227	Alpha-2-HS-glycoprotein alpha and beta chain	0.528 -0.366	-0.135 0.026	-0.155	0.463	-0.461	0.626	
	ALPHA-2-MACROGLOBULIN PRECURSOR	-0.277	-0.062	-0.054	-0.005	-0.160	0.568	
T68859	Alpha-2-plasmin inhibitor (alpha-2-PI)	0.312	0.222	0.317	0.952	0.878	0.718	
AA495869	ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM	-0.235	0.027	0.259	0.147	0.463	0.687	
	ALPHA-AMYLASE 2B PRECURSOR	-0.255	-0.156	D.066	0.239	0.313	0.436	
	ALPHA-CENTRACTIN	-0.228	1.308	-0.408	0.527	0.276	1.014	
T59043	Alpha-fetoprotein	0.195	0.354	0.282	0.144	0.142	0.529	
AA251784	ALPHA-GALACTOSIDASE A PRECURSOR	-0.135	-0.001	-0.121	-0.150	-0.142	0.040	
	Alternative guarine nucleotide-binding regulatory protein (G) alpha-inhibitory-subunit	0.334	0.528	0.294	0.222	0.671	0.188	
W42849	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR	-0.585	0.149	0.111	-0.331	0.322	-0.091	
T46924	Amiloride binding protein 1 (amine oxidase (copper-containing))	0.203	0.193	0.258	-0.032	0.349	0.204	
N50959	Amine oxidase, copper containing 2 (retina-specific)	0.022	0.681	-0.202	0.180	0.103	0.639	
	Amino acid transporter, cationic 2	1.018	0.487	1.245	1.419	1.369	0.185	
	AMINOACYLASE-1	-0.383	-0.213	-0.105	0.148	-0.114	0.351	
AA447761	Aminolevulinate, delta-, synthase 1	-0.001	-0.113	-0.092	0.236	0.372	0.602	
	Aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	-0.197	0.090	0.361	0.583	-0.003	0.792	
	AMP DEAMINASE 2 Amphiphysin (128kD autoantigen)	-0.626	-0.538	-0.105	0.076	-0.680	0.625	
H06483	Amphiregulin (schwannoma-derived growth factor)	0.243	1.153	0.168	0.112	1.761	1.024	
	Amylase, alpha 2A; pancreatic	-0.697	-0.323	-0.194	-0.277	0.206	0.645	
AA844818	Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage	-0.374	0.393	-0.052	0.637	0.530	0.320	
	Amyloid beta (A4) precursor-like protein 2	0.016	-0.359	-0.078	-0.175	0.137	-0.006	
H89517	Amyloid Deta (A4) preconsorting protein 2	-0.152	0.047	0.117	0.503	0.020	0.064	
R98019	ANGIOTENSIN-CONVERTING ENZYME PRECURSOR, SOMATIC	0.306	0.619	0.415	0.702	0.433	0.543	
	Ankyrin 1, erythrocytic	0.024	0.206	-0.202	-0.268	-0.484	0.768	
	Ankyrin 2 (neuronal)	-0.193	0.352	0.535	-0.278	-0.472	-0.019	
AA677185		-0.327	0.198	0.098	0.562	0.591	-0.390	
H63077	Annexin I (lipocortin I)	-0.018	0.360	-0.509	0.005	-0.293	-0.359	
	Annexin IV (placental anticoagulant protein II)	0.360	0.810	0.308	0.759	0.822	0.538	
	Annexin V (endonexin II)	-0.715	-0.335	0.022	0.463	0.157	0.438	
	Annexin VI (p68)	-0.480	-0.210	-0.033	-0.553	-0.043	0.772	
H15446	Annexin VII (synexin)	-0.195	-0.242	0.190	0.099	-0.330	-0.261	
	Annexin VIII	-0.499	-0.209	0.084	0.293	-0.332	0.190	
	Annexin XI (56kD autoantigen)	-0.327	-0.065	0.052	0.360	-0.252	-0.175	
AA884167	ANNEXIN XIII	-0.183	0.523	0.457	0.465	0.174	0.383	
AA937895	Antigen identified by monoclonal antibodies 12E7, F21 and O13	1.113	0.386	0.319	1.138	1.935	0.787	
AA630794	Antigen identified by monoclonal antibodies 4F2, TRA1.10, TROP4, and T43	-0.562	-0.159	0.038	0.520	0.250	0.810	
AA426264	Antigen identified by monoclonal antibody Ki-67	-0.407	-0.274	0.071	0.264	-0.394	0.793 0.291	
AA487429	ANTIGEN PEPTIDE TRANSPORTER 1	2.399	0.871	0.353	1.620	0.893	0.291	
AA683520	ANTILEUKOPROTEINASE 1 PRECURSOR	0.854	0.920	0.714	0.997	0.550 -0.310	0.644	
AA102646	Antiquitin	-0.067	-0.169	-0.055	-0.188	0.042	0.778	
T62060	Antithrombin III	0.140	0.271 0.352	0.343 0.336	0.243 -0.183	0.042	0.419	
AA478273	APEX nuclease (multifunctional DNA repair enzyme)	0.117 -0.225	-0.094	0.146	0.296	-0.278	0.150	
H49455	Apical protein (Xenopus laevis-like)	1.040	1.237	0.497	0.935	0.394	0.348	
	APK1 antigen	0.276	-0.160	-0.323	-0.465	-0.262	0.644	
	Aplysia ras-related homolog 12	0.148	-0.254	-0.071	0.516	-0.362	0.867	
H93332	Apolipoprotein B (including Ag(x) antigen)	-0.309	0.189	-0.199	-0.262	0.458	0.659	
	Apolipoprotein CI	0.023	0.054	-0.487	0.252	0.018	0.715	
	Apolipoprotein C-II	-0.113	-0.328	-0.066	0.211	-0.459	0.766	
	Apolipoprotein C-III	0.634	1.199	0.566	0.326	0.350	0.702	
T71887	Apolipoprotein C-IV Apolipoprotein D	0.122	0.509	0.814	1.440	0.111	0.724	
	Apoptosis (APO-1) antigen 1	0.381	1.023	0.507	1.467	0.634	0.655	
N46843	Aquaporin 4	0.307	0.452	0.016	0.189	0.449	0.783	
	Aquaporin 5	0.153	0.247	0.243	-0.016	-0.092	1.229	
H27752	Aquaporin 9	-0.451	-0.263	-0.586	-0.126	0.657	0.982	
H24316	AQUAPORIN-CHIP	-0.073	0.095	0.230	0.394	0.215	0.480	
T97276	Arachidonate 12-lipoxygenase	0.499	0.111	0.101	0.264	0.373	0.174	
H51574	Arachidonate 5-lipoxygenase	0.131	0.162	0.146	-0.072	-0.421	0.562 0.589	
AA598401	Archain	0.621	0.537	0.198	-0.290	0.806 -0.397	0.589	
AA447741	Arginase, liver	-0.122	0.096	0.022	-0.150 0.300	0.371	0.670	
H17612	Arginase, type II (non-hepatic)	0.568	0.792	0.058	0.300	0.463	-0.056	
AA679422	Arginine carboxypeptidase (carboxypeptidase N)	0.325	0.480	0.309	0.253	-0.144	0.684	
	Arginine vasopressin receptor 1 (AVPR1)	0.130	0.244 0.423	0.093 0.269	-0.003	0.605	0.824	
	Argininosuccinate lyase	0.118 0.265	0.423	0.063	0.315	0.503	0.946	
	Argininosuccinate synthetase	0.265	0.526	0.826	0.615	0.320	1.040	
	Arginyl-tRNA synthetase	0.595	1.057	0.186	0.082	0.558	0.955	
T67552	Aryl hydrocarbon receptor nuclear translocator	0.293	0.387	0.089	0.317	0.653	0.447	
	Arylacetamide deacetylase (esterase)	0.272	-0.744	-0.709	-0.065	-0.529	0.391	
T67128	ARYLAMINE N-ACETYLTRANSFERASE, MONOMORPHIC	0.322	0.138	0.055	0.206	-0.062	0.515	
H45449	Arylsulfatase A	0.513	0.737	0.505	0.139	0.230	0.866	
	Arylsulfatase B	0.599	0.046	0.240	0.786	0.568	0.759	
	Arylsulfatase D	0.216	0.358	-0.075	0.306	0.095	0.713	
H58255	Asialoglycoprotein receptor 1	0.952	0.019	-0.177	-0.296	-0.094	-0.142	
R98050	Asialoglycoprotein receptor 2	-0.429	-0.443	-0.116	-0.823	-0.134	-0.274	
	Asparagine synthetase Aspartoacylase (aminoacylase 2, Canavan disease)	0.211	0.673	-0.115	0.748	-0.062	0.828	
N71653	Aspartoacylase (aminoacylase 2, Carlavan disease) Aspartylglucosaminidase	0.471	0.748	0.562	0.887	0.298	0.869	
N51521	ASPARTYL-TRNA SYNTHETASE	0.190	0.144	0.076	1.102	0.439	0.425	
AA01835	ASPARTE-TROUGHTHE INSE Ataxia telangiectasia mutated (includes complementation groups A, C and D)	-0.198	0.025	-0.140	-0.155	-0.183	1.079	
AA256508		-0.173	0.601	-0.114	-0.160	0.026	0.380	
AA45883	ATL-derived PMA-responsive (APR) peptide	0.614	0.741	0.642	0.198	0.463	1.146	
AA136054	ATP citrate lyase	0.758	0.553	0.826	0.648	0.588	0.873	
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ACC Gene Name	ZR75	YY3	YY1	468	MPI	231 1.017	(log base 2 ratio
AA135824 ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR	-0.218 -0.523	-0.101 -0.046	0.324 -0.162	-0.204 -0.216	0.216 -0.046	1.005	
AA046701 ATP SYNTHASE LIPID-BINDING PROTEIN P1 PRECURSOR AA455126 ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR	-0.358	-0.665	-0.775	-0.715	-0.629	0.805	
AA504465 ATP synthase, H+ transporting, mitochondrial	0.454	0.250	0.686	0.091	0.833	0.442	
AA453765 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	-0.131 -0.438	-0.200 -0.170	-0.003 -0.039	-0.077 0.293	-0.066 0.426	0.124 0.604	
AA708298 ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide AA669314 ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	0.408	0.671	0.289	0.254	0.382	1.078	
AA873577 ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin se	ensitivity conferring -0.108	0.218	-0.024	0.059	0.695	1.237	
H85355 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0.020	-0.087	0.212 0.171	0.26B 0.256	-0.211 -0.105	1.146 0.663	
N93024 ATPase, Ca++ transporting, plasma membrane 4	-0.402 0.685	-0.270 0.553	0.521	0.328	1.007	0.970	
AA236141 ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome) N26536 ATPase, Cu++ transporting, beta polypeptide (Wilson disease)	0.578	0.493	0.129	0.204	0.528	0.754	
AA702541 ATPase, H+ transporting, tysosomal (vacuolar proton pump) 31kD	0.107	0.261	0.036	-0.111	0.239	0.925	
H05768 ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD	-0.247 kD. isoform 1 0.014	-0.374 0.313	0.067 -0.161	-0.677 -0.402	-0.526 0.264	1.123 0.760	
AA504160 ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70l AA877194 ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/5		0.472	-0.228	0.130	0.633	0.699	
AA873355 ATPase, Na+/K+ transporting, alpha 1 polypeptide	0.544	0.003	0.295	0.071	0.184	0.604	
R73570 ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	1.796	0.772	1.008 0.609	0.032 0.007	1.651 -0.297	1.005 0.520	
AA775957 ATPase, Na+/K+ transporting, alpha 3 polypeptide	0.687 0.259	0.826 0.326	0.264	0.405	0.438	0.701	
AA598814 ATPase, Na+/K+ transporting, beta 1 polypeptide H14808 ATPase, Na+/K+ transporting, beta 2 polypeptide	0.312	0.174	-0.250	-0.237	0.121	1.263	
H29521 ATP-binding cassette 3	0.608	0.712	0.353	0.349	0.789	0.724	
AA775355 ATP-DEPENDENT DNA HELICASE II, 86 KD SUBUNIT	0.203 0.857	0.466 0.656	-0.122 0.585	0.370 0.337	0.082 0.740	0.838 0.824	
AA448711 AU RNA-binding protein/enoyl-Coenzyme A hydratase AA454880 AU-rich element RNA-binding protein AUF1	0.170	0.259	0.120	0.115	-0.084	0.743	
AA487064 AUTOANTIGEN PM-SCL	-0.534	0.006	0.035	-0.242	-0.019	0.589	
AA479090 Autocrine motility factor receptor	-0.013	0.025	0.051	-0.059 -0.069	0.294 0.108	0.736 0.875	
R48232 Autosomal dominant polycystic kidney disease type II	-0.287 0.261	-0.034 0.500	0.050	0.085	0.397	0.449	
H15718 AXL receptor tyrosine kinase R40446 AXONIN-1 PRECURSOR	-0.185	0.368	0.124	0.140	0.225	0.662	
AA702802 Azurocidin 1 (cationic antimicrobial protein 37)	0.876	0.800	0.798	0.306	0.490	0.759	
W63749 B cell lymphoma protein 2	-0.019	0.210 0.334	0.186 0.586	-0.057 0.943	0.275 0.218	1.034 1.099	
R99926 B cell lymphoma protein 6 (zinc finger protein 51)	0.641 -0.085	0.334	0.305	0.100	0.339	0.682	
AA291513 B cell lymphoma protein 7B AA457114 B94 PROTEIN	-0.340	-0.277	0.060	-0.055	0.190	0.740	
AA680249 Bactericidal/permeability-increasing protein	-0.785	-0.820	-1.260	-0.810	-0.885	0.596	
R54846 Basic fibroblast growth factor (bFGF) receptor (shorter form)	0.717 0.354	0.404 0.276	0.035	0.494 0.141	0.391 -0.286	0.269 -0.068	
R83000 Basic transcription factor 3 AA455004 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT	-0.160	0.024	0.112	0.003	-0.052	0.677	
AA436440 Basigin	0.366	-0.626	-0.741	-0.859	0.160	1.137	
AA426216 BB1	1.583	1.002	1.767	1.141	2.192	0.209	
AA496678 B-cell CLL/lymphoma 3	0.036 -0.086	0.284 -0.023	0.215 0.199	0.452 0.539	-0.028 0.050	-0.411 -0.102	
N70463 B-cell translocation gene 1, anti-proliferative R05278 BETA-1,4 N-ACETYLGALACTOSAMINYLTRANSFERASE	-0.322	-0.023	-0.039	-0.181	-0.153	0.948	
R05278 BETA-1,4 N-ACETYLGALACTOSAMINYLTRANSFERASE AA670408 BETA-2-MICROGLOBULIN PRECURSOR	0.156	0.191	-0.282	0.151	0.198	0.787	
AA449982 Beta-A4 crystallin	-0.123	-0.174	-0.201	-0.194	0.083	1.048	
AA733203 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR	-0.504 0.619	0.298	0.278 0.640	-0.230 0.541	-0.011 0.851	0.749 1.111	
T58896 Betaine:homocysteine methyltransferase R55796 BETA-NEOENDORPHIN-DYNORPHIN PRECURSOR	0.040	0.048	0.913	0.599	1.364	1.087	
R55796 BETA-NEOENDORPHIN-DYNORPHIN PRECURSOR AA401441 B-factor, properdin	-0.038	0.007	-1.112	-0.290	-0.598	0.809	
N51018 Biglycan	0.016	0.098	0.330 0.122	-0.005 0.067	0.022 0.319	1.320 1.417	
AA406571 Biliary glycoprotein	0.567 -0.331	0.337 0.150	-0.069	-0.075	-0.240	1.295	
AA418045 BINDING REGULATORY FACTOR R17765 Biotinidase	-0.515	-0.014	-0.413	-0.604	-0.566	0.236	
R56774 Bone morphogenetic protein 1	0.020	0.431	-0.157	-0.537	-0.198 0.551	0.765	
AA489383 Bone morphogenetic protein 2	0.706 -0.327	0.519 -0.390	0.385 -0.197	0.254 -0.285	-0.311	-0.001	
AA463225 Bone morphogenetic protein 4 W73473 Bone morphogenetic protein 7 (osteogenic protein 1)	0.274	0.222	-0.065	0.197	0.309	1.132	
AA779480 Bone morphogenetic protein 8 (osteogenic protein 2)	0.267	-0.025	0.379	0.273	0.064	1.116	
N20203 Bone morphogenetic protein receptor, type II (serine/threonine kinase)	-0.179 0.259	-0.021 0.315	-0.041 0.217	-0.230 0.062	0.159 0.529	0.974 0.928	
AA194043 Bradykinin receptor B2 AA875888 BRAIN NEURON CYTOPLASMIC PROTEIN 1	-0.284	-0.211	-0.086	-0.283	-0.472	1.407	
AA452826 BRAIN SPECIFIC POLYPEPTIDE PEP-19	0.414	0.166	0.268	-0.026	0.366	1.201	
AA262988 Brain-derived neurotrophic factor	-0.149	-0.096	0.021	-0.280 -0.198	0.098 1.070	1.299 1.265	
AA436410 Branched chain aminotransferase 2, mitochondrial AA477298 Branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine	0.276 e disease) 0.084	0.219 0.264	0.400 0.120	0.403	0.272	1.282	
AA427739 Branched chain keto acid dehydrogenase E1, aprila polypeptide (maple syrup urine		0.272	0.328	0.453	0.252	1.195	
AA419342 Breakpoint cluster region protein BCR	-0.582	-0.347	-0.630	-0.862	-0.619	1.298	
H90415 Breast cancer 1, early onset	-0.226 0.731	0.195 0.056	0.143 -0.173	-0.069 0.065	0.350 0.261	1.013 0.584	
H48122 Breast cancer 2, early onset AA454222 Bromodomain, testis-specific	0.623	0.739	0.371	0.848	0.807	0.802	
AA629542 Brush-1	-0.543	-0.088	0.165	-0.113	-0.089	0.946	
H87536 Bullous pemphigoid antigen 2 (180kD)	0.038 -0.351	0.347 -0.289	-0.088 -0.003	0.157 -0.540	0.262 0.198	1.517 0.561	
AA885311 Butyrylcholinesterase AA633577 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC	0.395	-0.043	0.069	0.396	-0.078	0.911	
H81200 C4/C2 activating component of Ra-reactive factor	-0.322	0.044	0.118	0.086	0.376	1.247	
R85414 CAD PROTEIN	0.183	0.418	0.374	0.344	0.154	1.344 0.697	
AA136983 Cadherin 11 (OB-cadherin)	0.157 0.089	0.426 0.011	0.710 0.281	0.305 -0.165	0.916 0.632	0.817	
W49619 Cadherin 2, N-cadherin (neuronal) AA425217 Cadherin 3 (P-cadherin)	-0.043	0.607	0.515	0.079	0.571	0.696	
H02884 Cadherin 5 VF-cadherin (vascular epithelium)	0.692	0.115	0.362	0.280	0.482	0.770	
R98242 CAG-ist 7 (trinucleotide repeat-containing sequence) [human, pancreas, mRNA Pa	rtial, 701 nt] -0.050 -0.043	0.014 -0.205	0.166 -0.134	0.199 -0.100	0.093 -0.367	0.477 0.978	
H88329 CALBINDIN N89721 Calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt]	0.376	0.209	0.166	0.045	1.492	0.775	
N89721 Calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt] AA457092 Calcineurin B	1.235	0.151	0.910	0.838	0.704	0.904	
R14080 Calcium modulating ligand	-0.099	0.213	0.072	0.174	0.280	1.312 0.919	
AA455227 Calcium/calmodulin-dependent protein kinase IV	0.428 arathyroidism) 0.556	0.331 0.229	0.233 -0.080	-0.025 0.176	-0.075 0.512	1.304	
AA862999 Calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neonatal hyperpa AA076063 Caldesmon	-0.411	-0.523	-0.574	-0.196	-0.307	1.284	
AA039231 CALMODULIN-RELATED PROTEIN NB-1	0.021	0.132	0.164	0.829	-0.127	1.455	
AA126265 Calnexin	-1.181 0.100	-0.326 0.347	-1.793 0.087	-0.905 0.884	-1.001 0.082	0.238 -0.378	
H15456 CALPAIN 1, LARGE AA102454 Calpain, large polypeptide L2	0.100	0.642	-0.191	0.004	0.607	0.278	
AA102454 Calpain, large polypeptide AA676484 Calpain, small polypeptide	1.188	0.118	0.228	0.564	0.837	0.735	
AA416952 Calpastatin	-0.591	-0.390	0.030	-0.557	0.022	0.782	
AA043228 Calponin 3, acidic	-0.261 -0.262	-0.281 -0.184	-0.131 0.043	-0.310 0.208	-0.091 -0.467	0.630 0.799	
H99170 CALRETICULIN PRECURSOR AA484881 CAMP responsive element modulator	0.415	0.407	0.088	0.115	0.472	1.213	
AA630507 CAMP-dependent protein kinase regulatory subunit type I	0.615	0.239	0.169	0.089	0.771	1.103	
AA600217 CAMP-dependent transcription factor ATF-4 (CREB2)	0.666 0.433	0.212 0.325	0.388 0.278	0.487 0.079	0.334 0.578	1.387 1.315	
H12320 CAMP-RESPONSE ELEMENT BINDING PROTEIN	0.433	0.325	0.278	0.078	0.203	-0.134	
R20626 Cannabinoid receptor 1 (brain) AA486766 Capping protein (actin filament), gelsolin-like	0.680	0.623	0.625	-0.278	0.739	0.007	
T61078 Carbamoyl-phosphate synthetase 1, mitochondrial	1.379	0.835	0.322	-0.139	0.837	-0.567 0.354	
R93176 Carbonic anhydrase I	0.199 -0.188	0.111 0.113	0.262 -0.093	-0.009 -0.433	0.815 0.060	0.490	
H23187 Carbonic anhydrase II	3.133	, .					

ACC	Gene Name	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
AA481780	CARBONIC ANHYDRASE III	0.471 0.057	0.861 0.028	0.912 0.154	0.350 0.520	1.667 0.163	-0.077 0.239	
AA489653	Carbonic anhydrase IV Carbonic anhydrase VI	0.167	0.211	-0.062	0.053	0.448 -0.225	0.896 1.148	
AA280846 H91256	Carbonyl reductase Carboxyl ester lipase (bile salt-stimulated lipase)	0.277 -0.696	0.370 0.113	-0.082 -0.324	-0.168 -0.359	0.292	1.231	
AA058807	Carboxylestease 2 (liver)	0.538	0.077	0.308	0.030 0.114	0.390 0.137	0.693 0.247	
AA845178 T64223	Carboxypeptidase A1 Carboxypeptidase A3 (mast cell)	0.043	0.034 0.171	0.195	0.201	0.081	-0.223	
AA481513	Carboxypeptidase E	0.910	0.580	-0.116 0.949	-0.168 0.803	0.081 2.502	-1.381 0.068	
H61449	CARBOXYPEPTIDASE N 83 KD CHAIN CARCINOEMBRYONIC ANTIGEN PRECURSOR	0.914 0.628	0.567 0.371	0.204	0.459	-0.063	0.132	
AA487623	Cardiac gap junction protein	1.122	0.333	1.013 0.227	0.338 0.133	1.242 0.248	-0.322 -0.219	
AA621218 AA434115	Carnitine acetyltransferase CARTILAGE GLYCOPROTEIN-39 PRECURSOR	0.303 -0.336	-0.058	-0.024	-0.330	0.056	0.346	
AA427801	Cartilage linking protein 1	0.463 0.264	0.424 -0.060	0.395 -0.199	-0.398 -0.204	-0.054 0.156	0.618 0.873	
	Casein kinase 1, alpha 1 Casein kinase 1, epsilon	0.142	0.044	-0.112	0.149	0.157	0.359	
T98472	Casein kinase 2, alpha 1 polypeptide	-0.289 0.300	-0.084 0.422	0.355 0.198	0.254 0.310	0.499 0.558	0.945 0.851	
	Casein kinase 2, alpha prime polypeptide Casein kinase 2, beta polypeptide	0.108	1.346	-0.178	-0.158	-0.153	0.860	
H15685	Catalase Catechol-O-methyltransferase	0.092 0.207	0.312 0.051	0.549 -0.526	0.196 -0.412	0.690 -0.242	0.495 0.246	
AA676957	Catenin (cadherin-associated protein), alpha 1 (102kD)	0.568	-0.053	0.226	0.440	0.309	0.626 0.268	
	Catenin (cadherin-associated protein), beta 1 (88kD)	-0.050 0.265	-0.435 0.335	-0.369 0.265	-0.566 0.290	-0.202 0.256	0.200	
	Cathepsin B Cathepsin C	0.916	0.592	-0.010 0.249	0.464 0.192	0.743 -0.155	0.684 1.111	
N20475 H94487	Cathepsin D (lysosomal aspartyl protease) - Cathepsin E	-0.155 0.270	-0.054 1.308	0.561	0.782	0.102	1.037	
W92603	Cathepsin G	-0.326 0.338	-0.354 -0.158	0.188 0.383	0.795 -0.353	-0.398 0.251	0.138 0.728	
AA487231 R00859	CATHEPSIN H PRECURSOR CATHEPSIN K PRECURSOR	-0.902	-0.231	-0.439	-1.042	-0.739	0.064	
W73874	Cathepsin L	0.076 0.228	0.156 0.341	-0.345 -0.196	-0.055 0.518	0.370 0.004	1.080 0.410	
W07805 AA236164	CATHEPSIN O PRECURSOR CATHEPSIN S PRECURSOR	-0.098	-0.770	0.185	-0.618	0.024	0.487	
AA055835	Caveolin, caveolae protein, 22kD	-0.130 -0.256	0.192 0.140	0.023 -0.105	0.052 0.134	0.595 -0.109	0.417 0.533	
H58254 N20996	C-C CHEMOKINE RECEPTOR TYPE 2 CCAAT BOX-BINDING TRANSCRIPTION FACTOR 1	-0.201	0.095	0.114	-0.045	-0.018	0.710	
AA676804	CCAAT/enhancer binding protein (C/EBP), gamma	-0.175 0.305	-0.523 0.439	-0.452 0.779	-0.423 0.581	0.223 0.559	0.716 0.797	
	CD1c antigen (thymocyte antigen) CD1D antigen, d polypeptide	0.584	0.124	0.504	0.501	0.627	0.996	
N91385 N53534	CD20 RECEPTOR CD22 antigen	0.303 -0.767	0.248 -0.040	0.209 -0.697	-0.132 -0.785	-0.188 -0.720	0.441 1.039	
AA147594	CD30L RECEPTOR PRECURSOR	0.383	0.310	0.310 0.033	0.306 -0.383	0.444 -0.080	0.717 0.514	
AA434387 N39161	CD34 antigen (hemopoietic progenitor cell antigen) CD36 antigen (collagen type I receptor, thrombospondin receptor)	-0.211 0.051	0.025	0.100	-0.069	0.147	0.389	
AA676453	CD37 antigen	0.242 0.671	0.106 0.318	0.322 0.714	0.123 0.321	0.247 0.998	0.623 0.775	
R00276 H13211	CD38 antigen (p45) CD39 antigen	-0.103	-0.172	0.242	-0.034	-0.082	1.043	
T66799	CD3G antigen, gamma polypeptide (TiT3 complex)	-0.310 -0.101	-0.320 0.063	0.145 0.029	-0.415 0.287	-0.116 0.067	0.918 1.047	
H98636 AA283090	CD40L RECEPTOR PRECURSOR CD44 antigen (cell adhesion molecule)	1.229	0.622	0.954	0.049	0.571	0.730	
AA455448	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	-0.530 -0.203	-0.164 0.202	-0.294 -0.251	-0.435 -0.158	-0.171 0.125	0.303 0.304	
R05416 AA132090	CD48 antigen (B-cell membrane protein) CD53 antigen	0.487	0.854	0.574	0.109	0.725	0.236	
AA136271	CD58 antigen, (lymphocyte function-associated antigen 3) CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G34	0.434 0.580	0.267 0.016	0.483 0.452	0.127 0.119	0.745 0.366	0.558 0.797	
H60549 AA454563	CD63 antigen (melanoma 1 antigen)	0.134	0.998	-0.258	-1.013	1.035 0.757	0.774 1.136	
AA421296	CD68 antigen CD69 antigen (early T cell activation antigen)	0.491 0.153	-0.133 0.266	0.622 1.077	0.514 0.290	1.369	0.790	
AA812996	CD72 antigen	0.186 0.246	0.315 -0.155	0.165 0.631	0.258 -0.009	0.480 0.388	1.121 0.615	
AA443584 AA486556	CD8 antigen, alpha polypeptide (p32) CD81 ANTIGEN	0.351	0.448	0.218	0.396	0.395	0.274	
AA111969	CD83 ANTIGEN PRECURSOR	1.211 -1.625	1.522 -1.432	0.537 -1.398	-0.457 -2.122	-0.314 -1.693	0.702 0.512	
	CD9 antigen CDC21 HOMOLOG	2.482	0.492	1.956	1.711	2.352	0.603	
AA459292	CDC28 protein kinase 1	-0.317 -0.006	-0.181 -0.067	0.151 0.188	-0.279 -0.403	-0.530 -0.006	0.543 0.707	
	CDC28 protein kinase 2 CDC46 HOMOLOG	0.314	0.158	0.125	0.079	0.440	0.606	
AA164705	CDW52 antigen (CAMPATH-1 antigen)	0.423 0.387	0.485	0.567 0.456	1.480 0.605	0.362 0.689	0.826 0.896	
AA633993	CELL ADHESION PROTEIN Cell division cycle 10 (homologous to CDC10 of S. cerevisiae	-0.190	0.042	0.151	-0.089	0.428 0.318	0.910	
AA598974 W95001	Cell division cycle 2, G1 to S and G2 to M Cell division cycle 25C	-0.339	0.077	-0.082 -0.175	-0.309 -0.177	0.458	0.868	
T81764	Cell division cycle 27	-0.406 0.810	-0.023 0.452	-0.136 0.843	-0.305 0.593	-0.018 0.949	0.569 0.342	
AA668681 AA427934	Cell division cycle 42 (GTP-binding protein, 25kD) Cell division cycle 42 (GTP-binding protein, 25kD)	-0.294	0.153	-0.053	0.011	0.280	-0.375	
R59697	CELL DIVISION PROTEIN KINASE 8	0.191 0.920	0.149 1.078	0.045 0.629	0.137 -0.197	0.101 0.299	0.391 0.442	
N93505 AA625995	CELL SURFACE GLYCOPROTEIN A15 CELLULAR NUCLEIC ACID BINDING PROTEIN	-0.261	0.425	0.138	-0.045	-0.132	0.448	
AA454702	Cellular retinoic acid-binding protein [human, skin, mRNA, 735 nt]	0.611 0.530	0.432 0.465	0.255 -0.124	-0.196 -0.016	-0.006 0.094	1.016 0.892	
	Cellular retinol-binding protein Centromere autoantigen C	0.549	0.645	0.566	0.355	1.048	0.842	
	Centromere protein B (80kD) Centromere protein E (312kD)	0.609	0.299 0.152	0.408	0.202 0.452	0.838 0.263	0.841 0.876	
AA074613	Cerebellar degeneration-related protein (62kD)	1.447	0.905	0.597	0.468	0.259 0.065	0.829 0.696	
AA425008 W37753	CEREBELLIN 1 PRECURSOR Ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-vogt disease)	-0.110 0.302	0.063 -0.025	0.039 -0.312	0.051 -0.290	-0.044	-0.531	
H86554	Ceruloplasmin (ferroxidase)	0.742	0.594	0.477 0.345	0.261 -0.299	0.612 0.058	-0.403 0.708	
	CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME Chaperonin containing T-complex subunit 6	-0.138 0.250	0.206 0.166	-0.135	-0.265	-0.134	0.715	
R09220	Charot-Leyden crystal protein	0.321	0.153	0.141 0.426	0.300 0.116	0.214 0.753	0.564 0.583	
N74383 AA036881	Chediak-Higashi syndrome 1 Chemokine (C-C) receptor 1	0.583 0.623	0.371 0.442	0.181	0.110	0.758	0.732	
N51278	Chemokine receptor-like 1	0.560 0.303	0.406 0.248	0.470 0.127	0.109 0.249	1.061 0.379	1.009 0.971	
	Chitinase 1 5 Chloride channel 4	0.298	0.396	0.056	0.165	0.569	1.005	
R19276	Cholesteryl ester transfer protein, plasma	1.454 1.365	0.122 0.802	1.315 1.313	1.469 0.726	1.671 1.430	0.590 1.753	
H09959 R56604	Choline kinase Cholinergic receptor, nicotinic, alpha polypeptide 4	-0.266	-0.076	0.103	0.273	-0.075	0.780	
W93369	Cholinergic receptor, nicotinic, alpha polypeptide 7 Cholinergic receptor, nicotinic, epsilon polypeptide	0.443 0.607	1.103 0.513	-0.012 0.256	-0.263 0.499	0.320 0.742	-0.125 0.218	
R02059 N32604	CHORIOGONADOTROPIN BETA CHAIN PRECURSOR	0.414	0.757	0.475	-0.127 0.094	0.724 0.916	0.919 0.728	
R36264 W37769	Chromogranin A (parathyroid secretory protein 1) Chromogranin B (secretogranin 1)	0.179 0.313	0.497 0.088	0.205 0.174	-0.298	0.762	0.752	
AA291398	3 Chromosome condensation 1	1.813 0.305	0.496 0.214	0.177 0.097	-0.039 -0.095	0.022 -0.183	0.670 0.733	
AA463492	2 Chronic granulomatous disease	0.303	U.a. 14	0.001	5.000			

		ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
ACC	Gene Name Chymotrypsin-like	0.103	-0.535	-0.166	0.053	0.078	0.906	(108 DESC E 18110
	Chymotrypsin-like Chymotrypsinogen B1	-1.155	-0.568	-1.052	-1.065	-0.531	1.053	
H42728	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR	0.037	0.074	0.047	0.064	0.351	0.946	
AA708816	Clathrin heavy chain (alternative products)	0.169	-0.060	0.210 0.184	0.925 0.255	-0.102 0.642	0.419 0.358	
	Clathrin light chain A	0.620 0.517	0.508	0.083	0.285	0.596	0.072	
N20335 N52267	Clathrin, light polypeptide (Lcb) Clathrin-associated/assembly/adaptor protein, large, beta 1	0.594	0.400	0.167	0.160	0.655	0.244	
	CLEAVAGE SIGNAL-1 PROTEIN	0.678	0.043	-0.142	0.445	0.036	0.524	
W72816	Cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kD	0.354	0.268	0.025 -0.290	0.067 0.060	0.680 -0.665	0.584 0.780	
AA293218	Cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kD	0.078 0.457	-0.219 0.585	0.310	0.440	0.915	0.498	
AA700556	Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD Clusterin (complement lysis inhibitor; testosterone-repressed prostate message 2; apolipoprotein J)	-0.626	-0.352	-0.253	-0.159	0.527	0.619	
AA455910	Coagulation factor II (thrombin) receptor	0.703	0.757	0.453	0.159	1.006	0.635	
	Coagulation factor V	0.611	0.510	0.395	0.704	0.896	0.960 1.228	
N98524	COAGULATION FACTOR X PRECURSOR	0.055 0.719	-0.124 0.627	-0.108 0.252	-0.296 0.426	0.094 0.692	-0.154	
N52835	Coagulation factor XI (plasma thromboplastin antecedent)	0.378	0.324	0.340	0.281	0.318	0.297	
AA449742 T53792	Coagulation factor XIII, A1 polypeptide COATOMER BETA' SUBUNIT	0.364	0.090	-0.010	0.044	0.009	0.425	
T54662	COLIPASE PRECURSOR	-0.011	0.124	-0.086	0.077	0.230	0.762	
	Collagen, type I, alpha-2	-0.338	0.342	-0.996 -0.222	-0.066 0.103	-0.104 0.103	0.378 0.654	
N66737	Collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital)	0.014 1.655	0.550 0.767	0.819	0.103	2.082	0.559	
	Collagen, type IV, alpha 1	0.290	-0.079	0.021	-0.072	0.491	0.636	
H68555	Collagen, type IV, alpha 2 Collagen, type IV, alpha 4	0.498	0.687	0.069	0.311	0.681	0.823	
R61163	Collagen, type IV, alpha 5 (Alport syndrome)	-0.599	0.003	-0.562	-0.437	-0.482 -0.095	0.657 1.022	
AA496735	Collagen, type IX, alpha 3	-0.592 -1.048	-0.059 -0.371	0.127 -0.937	-0.025 -0.888	-0.800	0.541	
	Collagen, type V, alpha	0.479	0.610	0.263	0.304	0.847	0.569	
R75635 H99676	Collagen, type V, alpha 1 Collagen, type VI, alpha 1	0.184	0.159	0.000	0.199	0.019	0.576	
	Collagen, type VI, alpha 2	0.237	0.721	-0.052	0.382	0.591	0.434	
R31701	Collagen, type XI, alpha 1	0.340	0.421 0.971	-0.044 0.610	0.072 0.252	0.339 1.081	0.640 0.720	
AA455157	Collagen, type XV, alpha 1	0.917 0.687	0.421	-0.089	-0.063	0.555	0.528	
N81029	Collagen, type XVIII, alpha 1 Collapsin response mediator protein 1	0.514	-0.026	0.175	0.028	0.590	0.410	
AA870279 AA284954	Colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homo	0.763	0.574	0.268	-0.110	0.401	0.261	
AA458507	Colony stimulating factor 3 receptor (granulocyte)	0.160	-0.102	-0.615	-0.432	0.051	0.359	
T55558	Colony-stimulating factor 1 (M-CSF)	-0.356 -0.097	-0.006 -0.115	0.014 0.150	0.031 0.229	0.411 0.260	0.608	
AA873152	COMPLEMENT C3 PRECURSOR Complement component (3d/Epstein Barr virus) receptor 2	0.596	1.251	0.542	0.406	0.571	0.843	
AA521362	Complement component 1 inhibitor (angioedema, hereditary)	0.165	0.198	0.072	-0.025	0.452	0.143	
T71284	Complement component 1, q subcomponent, beta polypeptide	0.461	0.682	-0.291	0.318	0.703	-0.402	
T62048	Complement component 1, s subcomponent	0.978	0.564 0.256	-0.287 0.058	0.552 0.042	-0.012 0.254	0.327 0.058	
	Complement component 4A	0.244 0.092	-0.261	0.067	0.184	-0.059	-0.018	
T62036	Complement component 4-binding protein, alpha Complement component 4-binding protein, beta	0.252	0.387	0.175	0.486	0.656	0.629	
AA677687 N59396	Complement component 6	-0.020	0.671	-0.408	-0.129	0.651	0.489	
	Complement component 7	0.099	-0.123	-0.410 -0.440	-0.218 -0.407	-0.431 0.282	-0.254 0.216	
H53865	Complement component 8, alpha polypeptide	-0.093 0.410	0.140 0.420	-0.058	-0.056	-0.189	-0.460	
T68274	Complement component 8, beta polypeptide	0.206	0.373	0.081	0.432	0.337	0.486	
T69603 T71879	Complement component C1r Complement component C2	0.879	0.725	0.268	0.272	0.325	0.386	
N53664	Complement component C5	0.165	0.398	0.125	0.176	0.777	-0.098 0.333	
T74567	COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR	-0.005 0.781	0.295 0.599	-0.137 0.356	0.243 0.384	0.196 0.370	0.058	
W92812	Connective tissue activation peptide III	0.675	0.929	0.453	0.552	0.334	-0.030	
H20658	Connective tissue growth factor Contactin 1	-0.558	-0.628	-1.103	-0.373	0.303	0.149	
AA700808	Coproporphyrinogen oxidase (coproporphyria, harderoporphyria)	0.387	0.403	0.501	0.281	0.772	0.797	
AA187148	Core-binding factor, beta subunit	-0.070 -0.282	-0.183 0.119	-0.296 -0.246	-0.304 -0.424	-0.169 -0.344	0.630 1.097	
	CORTICOSTEROID 11-BETA-DEHYDROGENASE, ISOZYME 1	0.414	0.300	0.143	0.393	0.775	0.603	
H90764 H07089	Corticosteroid binding globulin CORTICOTROPIN RELEASING FACTOR RECEPTOR 1 PRECURSOR	0.595	0.431	-0.284	-0.679	0.705	0.017	
	COUP TRANSCRIPTION FACTOR	0.254	0.261	0.027	0.116	0.342	-0.309	
T97615	C-reactive protein	-0.273	0.300 -0.146	-0.122 -0.368	0.073 -0.487	-0.465 -0.017	0.521 -0.102	
	Creatine kinase B	-0.553 0.048	0.242	-0.174	0.313	-0.144	-0.001	
	Creatine kinase, mitochondrial 2 (sarcomeric) Crystallin beta-B2	0.067	0.548	0.448	0.109	0.789	0.169	
R59968	Crystallin Mu	0.135 .	0.015	-0.050	0.177	0.520	0.624	
R40945	Crystallin zeta (quinone reductase)	0.369	0.524 0.013	0.084 0.402	-0.091 0.256	0.872 0.741	0.482 0.817	
	Crystallin, alpha B	0.154 -1.936	-1.665	-1.439	-1.815	-1.690	0.783	
H09614	CTP synthetase Cut (Drosophila)-like 1 (CCAAT displacement protein)	0.037	0.108	0.222	0.125	0.167	0.754	
W93472	Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)	0.357	0.123	0.363	0.217	0.805	0.738	
H82536	Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)	0.356	0.217	-0.071 -0.165	-0.102 0.396	0.389 0.298	0.049 0.177	
AA608568		-0.069 0.535	0.905 0.234	0.340	-0.041	0.763	0.533	
R46787 AA487486	Cyclin B1 Cyclin D1 (PRAD1; parathyroid adenomatosis 1)	0.284	0.890	0.400	0.407	0.533	0.260	
H84154	Cyclin D2	0.895	0.761	0.284	0.212	0.080	0.081 0.630	
T54121	Cyclin E	-0.170 0.662	-0.262 0.615	-0.190 0.170	-0.314 0.174	0.140 0.191	0.426	
AA676797		-0.601	0.171	-0.238	0.192	0.517	0.759	
AA454146	Cyclin-dependent kinase 5, regulatory subunit	0.772	0.718	0.150	.0.292	0.297	0.558	
H73724	Cyclin-dependent kinase 6	0.427	-0.162	0.010	-0.182	-0.925	0.301	
R22625	Cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	0.547	0.754	-0.099 0.233	0.010 0.270	0.120 0.621	-0.368 0.156	
	Cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	0.596 0.100	0.448 0.553	0.206	0.240	0.120	0.627	
R07167	Cýstathionase (cystathionine gamma-lyase) CYSTATIN A	-0.504	0.250	0.051	-0.271	-0.005	-0.071	
W72207 H22919	CYSTATINB	0.168	-0.053	0.010	-0.043	0.278	0.201	
AA599177	Cystatin C (amyloid angiopathy and cerebral hemorrhage)	-0.218	0.250	0.112	0.145 0.222	0.864 0.393	0.381 0.621	
W72895		1.050 0.260	1.275 0.631	0.275 0.240	0.470	0.383	0.298	
	Cysteine dioxygenase, type 1 Cysteinyl-tRNA synthetase	1.674	2.002	0.994	0.566	2.176	0.530	
AA431125	Cysteinyl-trink synthetase Cytochrome b-245, alpha polypeptide	-0.017	0.103	0.088	-0.091	0.369	1.046	
R91950	Cytochrome b-5	0.364	0.613	0.050	0.046	0.024 0.467	0.562 0.153	
AA457700	Cytochrome B561	0.489 0.013	0.406 -0.085	-0.005 -1.012	0.170 -0.965	-0.447	-0.176	
R53311	CYTOCHROME C CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR	0.696	0.234	0.072	0.226	0.410	-0.356	
AA456931	CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR	0.873	0.383	0.936	0.322	1.328	-0.031	
AA862813	CYTOCHROME C OXIDASE POLYPEPTIDE VIII-LIVER/HEART PRECURSOR	-0.443	0.103	0.083	-0.238	0.496	-0.200	
N71160	Cytochrome c oxidase subunit VIb	0.039 0.462	-0.176 1.492	0.169 0.290	0.324 0.272	0.342 0.451	-0.303 0.555	
N56693	Cytochrome c oxidase subunit VIIb	0.462	0.823	-0.221	0.161	0.731	0.413	
N36299 AA629710	Cytochrome c oxidase subunit X (heme A: famesyltransferase Cytochrome c oxidase VIIc subunit	-0.058	-0.413	-0.019	-0.041	-0.446	0.354	
	4 Cytochrome c1	-0.144	-0.250	0.112	0.489	0.039	0.694	
R52654	Cytochrome c-1	-0.031 1.537	0.170 0.113	0.192 1.327	0.763 0.517	0.400 1.247	0.553 0.567	
AA88470	9 Cytochrome P450 11 beta	1.537 -0.217	0.060	0.047	0.402	0.399	0.310	
AA44815	7 Cytochrome P450 IB1 (dioxin-inducible)							

ACCOUNTS FAME FAM			ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
Continues Add in the original relations chan 19 122 103 10	ACC	Gene Name							(108 0200 2 1000
Section	AA873089								
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AMATISS Cythonic Pales 1,000 1		CYTOCHROME P450 IVB1 .		0.138					
Company Comp		Cytochrome P450 reductase [numan, placenta, mixina Partial, 2403 ft]		-0.484					
12020 Cyclochome FASE, authority 14, general controlled, polypoted 6 0.58 0.59 0.07 0.33 0.09 0.04		Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1							
Collections PUSS, Salabary IC (Ingressperion Appropriate)	T72259	Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6							
Discontinum Published Disc									
Company March Ma		Cytochrome P450, subfamily IIC (menhanytoin 4-hydroxylase)							
Medical Cyclestome FAIS, authority VIII, polipsychia 1.000		Cytochrome P450, subfamily ItJ (arachidonic acid epoxygenase) polypeptide 2		0.489					
Collections PLSS, actions you (Collections PLSS, actions) (Coll		Cytochrome P450, subfamily IVA, polypeptide 11							
Description Policy Leading 2011 2012 2013 2010 2014 2013 2010 2014 2013 2010 2014 2015 2014 2015 2014 2015 2014 2015 2014 2015		Cytochrome P450, subfamily XIX (aromatization of androgens)							
		Cytochrome P450, subfamily XVII (steroid 17-alpha-hydroxylase), adrenal hyperplasia							
AA460305 Demograph care product for the product of 127 ab 10 and		Cutochrome P450, subfamily XXVII (steroid 27-hydroxylase, cerebrotendinous xanthomatosis)			-0.003				
AMASSES DESCRIPTIONS FOR THE PROPERTY OF THE P	AA486393	Cytokine receptor family II, member 4							
AMASSES DEPOSITION CONTROL PROPERTIES AND CONTROL PROPERTIES PROPERTIES AND CONTROL PROPERT	AA410517	Cytoplasmic antiproteinase							
Delignar	AA608557	Damage-specific DNA binding protein 1 (127 kD)				0.042			
ROSSET Decay accelerating better for compelement (CDCs, Course blood group system) 0.111		Damage-specific DNA binding protein 2 (40 kD) D.RETA_HYDROXYRI ITYRATE DEHYDROGENASE PRECURSOR				0.048			
Additional Continue Continu		Decay accelerating factor for complement (CD55, Cromer blood group system)							
AA46800 Desprégrée finance 0.716 0.917 0.916 0.920 0.225 0	AA099394	Decorin							
Authorities									
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AMASSIS Desprishment in label AMASSIS Desprishment in label BESACTIVE AND INC. BESA	R07506	Deoxyguanosine kinase							
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Characteric Option Processing Number State Processin		Diacylglycerol kinase, alpha (80kD)							
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AAA4742 Directioncomined deshiftocomeses (El component of growth deshiftocomess commoner) Component of growth deshiftocomess commoners (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth deshiftocomes) Component of growth deshiftocomes (El component of growth d	R00884	Dihydrofolate reductase							
Available	AA447748	Dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate							
Add Company		Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)			0.024				
AA79250 DHYPROCROTATE DEHYPROCEMBARE PRECURSOR (1987) WASSES DHYPROCROTATE DEHYPROCEMBARE (1987) WASSES DHYPROCROTATE DEHYPROCROTATE (1987) WASSES DHYPROCROTATE (1987) WASSES DHYP	N29901	Dihydrolipoamide S-acetyltransferase (E2 component of 2-oxo-alutarate complex)					0.918		
MY280 DIPYOROPRYRIDMS-SENTIVE_LTYPE_CALCIUM CHANNEL GAMMA SUE 0.000 0.	AA173225	DIHYDROOROTATE DEHYDROGENASE PRECURSOR							
### STATES DISPONDERS SENSITIVE LTYPE: RECEITAL MUSICLE CALCIUM CHANNEL GOMEN 0.347 0.332 0.33		DINVIDEOR PRIDING SENSITIVE 1 TYPE CALCIUM CHANNEL BETA-1-81 SUBUNIT							
Real Bus Displacement with contents Co		DIHYDROPRYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUL							
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Web 197 Dispetisjepetisjes VI National Properties Nation		Dipentidylpentidase IV (CD26, adenosine deaminase complexing protein 2)	-0.202						
MASSES DIA Section repair protein ERCOS 0.518 0.001 0.118 0.550 0.464 0.465		Dipentidylpentidase VI							
AASS-100 Description Control									
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New Interpretation MLH 1.597 1.740 0.555 0.960 1.294 0.951									
MARSON Company Compa									
AA868125 DNA polymerase beta subunit AA868126 DNA polymerase beta subunit AA868126 DNA polymerase beta subunit AA868126 DNA polymerase gamma AA868127 DNA primase polypeptide 2A (580c) AA86812 DNA primase polype						0.217	-0.014		
AA88712 DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A 0.127 0.008 0.244 0.205 0.244 0.205 0.244 0.205 0.204 0.205 0.204 0.205	AA402855	DNA polymerase beta subunit							
AA182937 DNA polymane polypeptide (14pbC) A02937 DNA primane polypeptide (14pbC) A02938 DNA prim	AA680129	DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A							
AA4364G ID NA repair protein MSH2 AA364G ID NA repair protein MSH2 AA365G ID NA repair protein MSH2 AA464G ID NA-REPAIR PROTEIN NA AA464G ID NA-REPAIR PROTEIN NA AA464G ID NA-REPAIR PROTEIN NECA AA464G ID NA-REPAIR PROTEIN NECA AA468G ID NA-REPAIR PROTEIN NECA AA476G ID NA-REPAIR PROTEIN NECA AA468G ID NA-REPAIR PROTEIN NECA AA4									
Add						-0.476			
AA219061 DNA repair protein MSH2 0.218 0.229 0.429 0.429 0.421 0.209 0.099									
R39148 DNA repair protein ANCO-CA A023285 DNA repair protein ANCO-CA A023285 DNA spoisonements	AA219061								
AA45300 DNA-BINDING PROTEIN A -0.62 0.212 0.036 0.787 0.222 0.176									
AM-88121 DN-8-BINDING PROTEIN MEL-18 D.544 D.265 D.275 D.265 D.275 D.265 D.275 D.265 D.275 D.275 D.265 D.275 D.2			-0.624						
AM85214 DIAA-damage-inducible transcript Collect Coll	AA464421	DNA-BINDING PROTEIN MEL-18							
AA1-126 DNA-DIRECTED RNA POLYMERASE II 14.4 KD POLYPEPTIDE AA1-1688 DNA-DIRECTED RNA POLYMERASE II 14.4 KD POLYPEPTIDE AA1-17912 DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE AA1-17912 DNA-DIRECTED RNA POLYMERASE II 12.5 KD POLYPEPTIDE AA1-17912 DNA-PROTEIN HOMOLOG I AA1-17912 DNA-PROTEIN HOMOLOG II 1.0 LO A1-17912 DNA-PROTEIN HOMO	AA485214	DNA-BINDING PROTEIN NEFA PRECURSOR							
AA77192 DNA-DIRECTED RAN POLYMERASE II 13 KD POLYPEPTIDE 40.0030 0.0030	AA147214	DNA-gamage-inducible transcript 1					1.373	-0.649	
AA297042 DNA-DIRECTED RNA-POLYMERASE II 23 KD POLYPEPTIDE AA391758 DNAJ PROTEIN HOMOLOG 1 R45428 DNAJ PROTEIN HOMOLOG 1 R45428 DNAJ PROTEIN HOMOLOG BSJ1 AA26329 DNAJ PROTEIN HOMOLOG BSJ1 AA26329 DNAJ PROTEIN HOMOLOG BSJ1 AA26323 DNA-REPAIR PROTEIN KCOT AA45528 DNAJ PROTEIN HOMOLOG BSJ1 AA26323 DNA-REPAIR PROTEIN KCOT AA45528 DNAJ PROTEIN HOMOLOG BSJ1 AA26323 DNA-REPAIR PROTEIN KCOT AA45528 DNAJ PROTEIN HOMOLOG BSJ1 AA26323 DNA-REPAIR PROTEIN KCOT AA45528 DNA-REPAIR PROTEIN KCC1 AA45528 DNA-REPAIR PROTEIN KCC1 AA45638 DOA-REPAIR PROTEIN KCC1 AA45640 Doa-REPAIR PROTEIN KCC1 AA46640 DOA-REPAIR PROTEIN KCC1	AA777102	DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE							
AA491756 DNAJ PROTEIN HOMOLOG 1 AA55298 DNAJ PROTEIN HOMOLOG 9 AA55298 DNAJ PROTEIN HOMOLOG 18.1 AA267329 DNAJ PROTEIN HOMOLOG BL AA455298 DNAJ PROTEIN HOMOLOG BL AA267329 DNA PROTEIN HOMOLO	AA027042	DNA-DIRECTED RNA POLYMERASE II 23 KD POLYPEPTIDE							
MA3528 DNA PROTEIN HOMOLOG HSJ1 A48528 DNA PROTEIN HOMOLOG HSJ1 A287323 DNA PROTEIN HOMOLOG HSJ1 A287323 DNA PROTEIN ROMPLEMENTING XP-C CELLS D. 10.55 D. 10	AA481758	DNAJ PROTEIN HOMOLOG 1					0.044	1.261	
AA25132 DNA-REPAIR PROTEIN XCOMPLEMENTING XP-C CELLS AA25139 DNA-REPAIR PROTEIN XRCC1 AA405800 Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) A702640 Dopa decarboxylase (aromatic L-amino acid decarboxylase) A702640 Dopa-bratome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) A702640 Dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) A702640 Dopac	AA455298	DNAJ PROTEIN HOMOLOG 2	-0.170	0.345					
AAJ5139 DNA.REPAIR PROTEIN XRCC1 AAJ61890 Dodeceny-Ocenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A delta isomerase) Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A delta isomerase) Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A delta isomerase) Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A delta isomerase) Dodecenoyl-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dodecenoyl-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dodecenoyl-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dodecenoyl-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dodecenoyl-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dodecenoyl-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dodecoenvil-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dodecoenvil-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dodecoenvil-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dodecoenvil-Coenzyme A delta isomerase (4,0 and a delta isomerase) Dover-regulated and a delta isomerase (4,0 and a delta isomerase) Dover-regulated and a delta isomerase (4,0 and a delta isomerase (4,0 and a delta isomerase) Dover-regulated and a delta isomerase (4,0 and a delt	AA287323	DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS							
AA702640 Dopa decarboxylase (aromatic L-amino acid decarboxylase) AA702640 Dopa decarboxylase (aromatic L-amino acid decarboxylase) AA702650 Dopa decarboxylase (aromatic L-amino acid decarboxylase) AA702650 Dopa decarboxylase (aromatic L-amino acid decarboxylase) AA702650 Dopad-home tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) Down-regulator of transcription 1, TBP-binding (negative cofactor 2) -0.052	AA425139	DNA-REPAIR PROTEIN XRCC1							
AA39782 Dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) AA39782 Dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) AA600189 Double-stranded RNA adenosine deaminase AA3132007 Down-regulator of transcription 1, TBP-binding (negative cofactor 2) AA600189 Double-stranded RNA adenosine deaminase AA132007 Down-regulator of transcription 1, TBP-binding (negative cofactor 2) AA600189 DPH2L AA473080 DPH2L AA47470 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 AA25826 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA269383 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA269383 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY PROTEIN PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY PROTEIN PROSPHATASE PAC-1 AA490709 Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase DUAL SPECIFICITY PROTEIN PROTEIN PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY MITOGEN-	AA405800	Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)							
AA600189 Double-stranded RNA adenosine deaminase AA600189 Double-stranded RNA adenosine deaminase AA60180 Double-stranded RNA adenosine deaminase AA132007 Down-regulator of transcription 1, TBP-binding (negative cofactor 2) AA670380 DPH2L AA670380 DPH2L DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 AA25828 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA259280 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA759048 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759048 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759048 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759049 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759040 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE MINASE 3 AA759040 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE 3 AA759040 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE 3 AA759040 DUAL SPECIFICITY MITO	AA397824	Donachrome tautomerase (donachrome delta-isomerase, tyrosine-related protein 2)	-0.618	-0.478					
AA600199 Doube-stranded kniv a decirolism of a cell minuse of a A132007 Down-regulator of transcription 1, TBP-binding (negative cofactor 2) AA670380 DPH2L AA7430 DPH2L AA7430 DPL2L AA7430 DPL3 SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 AA25826 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA25826 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA25826 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA259383 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1 AA759046 DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1 AA497079 Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase DUTHy blood group AA480219 DUTP pyrophosphatase AA96334 DYNAMIN-1 AA66118 Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, E AA75904 Early growth response z (Krox-20 (Drosophila) homolog) AA480532 Early growth response protein 1 AA480533 Early growth response protein 1 AA480533 Early growth response protein 1 AA480534 Early growth response protein 1 AA480535 Early growth response protein 1 AA480535 Early growth response protein 1 AA406040 Edg-2 T66990 Egf-like module containing, mucin-like, hormone receptor-like sequence 1 -0.774 -0.480 -0.351 -0.322 -0.045 -0.057 -0.028 -0.072 -0.298 -0.072 -0.298 -0.072 -0.298 -0.072 -0.078 -0.072 -0.078 -0.079 -0.074 -0.070	AA478553	3 Dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)							
AA732007 Down-regulator of transcription 1, 15P-clinting (regalive Collection 2) AA670380 DPH2L R44740 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 AA428286 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA62383 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1 AA497079 Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase -0.176 0.078 0.024 0.406 0.107 1.070 Duffy blood group AA489219 DUTP pyrophosphatase -0.176 0.078 0.024 0.406 0.107 1.070 Duffy blood group AA489219 DUTP pyrophosphatase -1.661 -1.298 -1.172 -1.763 -0.754 0.976 AA4450118 Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, C -0.204 0.439 0.148 0.539 0.168 0.447 AA4450118 Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, C -0.204 0.439 0.148 0.539 0.168 0.447 AA468272 Early growth response 2 (Krox-20 (Drosophila) homolog) -0.544 -0.396 0.087 0.336 0.226 0.791 AA486533 Early growth response protein 1 -0.406 0.017 0.052 0.008 0.087 0.136 0.0161 -0.172 0.536 0.213 0.208 0.057 1.261 AA486530 Early growth response protein 1 -0.406 0.017 0.052 0.009 0.008 0.008 0.007 0.001 -0.407 0.001 0.002 0.000 0.002 0.000 0.0	AA600189	Double-stranded RNA adenosine deaminase							
AA750906 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 AA425826 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA25938 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA25938 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1 AA97079 Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase -0.315	AA132007	Down-regulator of transcription 1, TBP-binding (negative coractor 2)							
AA25828 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 AA259383 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 AA759046 DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1 AA497079 Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase Duffy blood group AA489219 DUTP pyrophosphatase AA498219 DUTP pyrophosphatase AA498219 DUTP pyrophosphatase AA498219 DUTP pyrophosphatase AA49833 DYNAMIN-1 AA461118 Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, E AA486532 E2F transcription factor 5, p130-binding AA4480219 E2F transcription factor 5, p130-binding AA4480219 E2F transcription factor 5, p130-binding AA4480219 E3F DA448027 E4F DA458025 E4F growth responses protein 1 AA466118 Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, E AA486533 Early growth responses protein 1 AA466110 E3F DA458025 E4F DA458025 E	R44740	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1							
AA59398 DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1 AA759046 DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1 AA759046 DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1 AA497079 Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase Duffy blood group Duffy blood group AA489218 DUTP pyrophosphatase -1.661 -1.298 -1.172 -1.763 -0.054 AA489334 DYNAMIN-1 AA48118 Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, E -1.661 -1.298 -1.172 -1.763 -0.754 AA455521 E2F transcription factor 6, p.130-binding AA480533 Early growth response 2 (Krox-20 (Drosophila) homolog) AA486533 Early growth response protein 1 -0.172 -0.536 -0.213 -0.206 -0.045 -0.101 1.521 AA486533 Early growth response protein 1 -0.172 -0.536 -0.031 -0.322 -0.045 -0.101 1.521 AA66640 Edg-2 T66980 Egf-like module containing, mucin-like, hormone receptor-like sequence 1 -0.744 -0.309 -0.545 -0.057 -0.05	AA425826	3 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2							
AA497079 Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase -0.176 0.076 0.078 0.024 0.406 0.107 1.070 T82477 Duffy blood group -0.070 0.001 0.062 0.514 -0.043 1.104 -0.070 0.001 0.062 0.514 -0.043 1.104 -0.070 0.001 0.062 0.514 -0.043 1.104 -0.070 0.001 0.062 0.514 -0.043 1.104 -0.070 0.001 0.062 0.514 -0.043 1.104 -0.070 0.001 0.062 0.514 -0.043 1.104 -0.070 0.001 0.062 0.514 -0.043 1.104 -0.070 0.001 0.062 0.514 -0.043 1.104 -0.070 0.001 0.062 0.514 -0.043 1.104 -0.070 0.001 0.062 0.514 -0.054 0.076 -0.070 0.001 0.062 0.0754 0.076 -0.070 0.001 0.062 0.065 0.0754 0.076 -0.070 0.001 0.062 0.065 0.065 0.065 -0.070 0.001 0.062 0.065 0.065 -0.070 0.001 0.062 0.065 0.065 -0.070 0.001 0.062 0.065 0.065 -0.070 0.001 0.062 0.065 0.065 -0.070 0.001 0.062 0.065 -0.070 0.001 0.002 0.001 0.062 0.065 -0.070 0.001 0.001 0.001 0.002 -0.070 0.001 0.001 0.001 0.001 0.001 0.001 0.001 -0.070 0.070 0.070 0.001 0.00	AA82938	B DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3							
T82477 Duffy blood group AA489219 DUTP pyrophosphatase AA49219 DUTP pyrophosphatase AA49234 DYNAMIN-1 AA45118 Dvstrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, E AA45518 Dvstrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, E AA45518 E2F transcription factor 5, p130-binding AA45017 E2F transcription factor 5, p130-binding AA46027 Early growth response 2 (Krox-20 (Drosophila) homolog) AA46532 Early growth response protein 1 AA46633 Early growth response protein 1 AA46634 Edg-2 T66980 Egf-like module containing, mucin-like, hormone receptor-like sequence 1 AB45015 Elastase 1, pancreatic (elastase IIA) AB45015 Elastase 1, pancreatic (elastase IIA) AA845167 ELASTASE IIIA PRECURSOR W45415 ELASTASE IIIB PRECURSOR T57919 Electron-transfer-flavoprotein, alpha polypeptide (glutaric acidurie III) AB48414 ELKI member of ETS procepus family -0.084 -0.164 -0.164 -0.322 -0.285 -0.581 -0.580 -0.597 -0.581 -0.767 -0.713 -0.237 -1.660 -0.025 -0.590 -0.085 -0.085 -0.085 -0.085 -0.085 -0.085 -0.086 -0.095 -0.087 -0.096 -0.096 -0.097 -0.096 -0.096 -0.096 -0.097 -0.096 -0.097 -0.096 -0.097 -0.096 -0.097 -0.096 -0.097 -0.096 -0.097 -0.096 -0.096 -0.097 -0.096 -0.096 -0.096 -0.096 -0.096	AA/5904	Dual-specificity tymsine-(Y)-phosphorylation regulated kinase		0.167	-0.459	-0.654			
AA48219 DUTP pyrophosphatase AA48219 DUTP pyrophosphatase AA48211 DyNAMIN-1 AA61118 Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, E AA65521 E2F transcription factor 8, p130-binding AA480532 E2F transcription factor 8, p130-binding AA480533 Early growth response 2 (Krox-20 (Drosophila) homolog) AA480533 Early growth response protein 1 AA406040 Edg-2 T6990 Egf-like module containing, mucin-like, hormone receptor-like sequence 1 C9744 -0.309 AA480543 Early growth cesponse protein 1 C9744 -0.309 AA480543 Early growth cesponse protein 1 C9744 -0.309 AA480543 Early growth cesponse protein 1 C9744 -0.309 AA480545 Elastase 1, pancreatic (elastase IIA) AA485567 Elastase 1, pancreatic (elastase IIA) AA485567 ELASTASE IIIA PRECURSOR AA485676 ELASTASE IIIA PRECURSOR AA845167 ELASTASE IIIB PRECURSOR BELASTASE IIIB PRECURSOR C9754 -0.106 C9754 -0.106 C9754 -0.107 C9754 -0.107 C9754 -0.107 C9755 -0.129 C9754 -0.107 C9754 -0.107 C9757 -0.129 C9754 -0.107 C9754 -0.107 C9757 -0.208 C9757 -0.129 C9757	T82477	Duffy blood group							
AA46334 DYNAMN-1 AA46118 Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, E AA46518 Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, E AA465521 E2F transcription factor 5, 1930-binding AA465521 E2F transcription factor 5, 1930-binding AA466532 Early growth response protein 1 AA466533 Early growth response protein 1 AA406404 Edg-2 AA406404 Edg-2 AA40640 Edg-2 AA406405 Egl-like module containing, mucin-like, hormone receptor-like sequence 1 AA406404 D340 AA406405 Elsatase 1, pancreatic (elastase IIA) AA406405 Elsatase 1, pancreatic (elastase IIA) AA406406 Elsatase 1, pancreatic (elastase IIA) AA406406 ELASTASE IIIA PRECURSOR W45415 ELASTASE IIIB PRECURSOR BLASTASE IIIB PRECURSOR CABABAGAGA ELASTASE IIIB PRECURSOR CABABAGAGA ELASTASE IIIB PRECURSOR ELASTASE IIIB PRECURSOR ELASTASE IIIB PRECURSOR CABABAGAGA ELASTASE IIIB PRECURSOR ELASTASE IIIB PRECURSOR ELASTASE IIIB PRECURSOR CABABAGAGA ELASTASE IIIB PRECURSOR ELASTASE IIIB PRECURSOR CABABAGAGA ELASTASE IIIB PRECURSOR ELASTASE IIIB PRECURSOR CABABAGAGA ELASTASE IIIB PRECURSOR CABABAGAGA ELASTASE IIIB PRECURSOR ELASTASE IIIB PRECURSOR CABABAGAGA ELASTASE IIIB PRECURSOR CABABAGAG	AA48921	DUTP pyrophosphatase							
AA45118 Dystrophin (intuscal dystrophin, Churchine and Section (April 2014) and Section (April 2	AA49633	4 DYNAMIN-1 P. Dystrophin (muscular dystrophy, Dyshenne and Becker types), includes DXS142, DXS164, DXS206, C.					0.168	0.417	
AA48027 Early growth response 2 (Krox-20 (Drosophila) homolog) AA4807 Early growth response 2 (Krox-20 (Drosophila) homolog) AA4807 Early growth response Protein 1 AA4807 Early Ea	AA45552	E2F transcription factor 5, p130-binding	-0.225	0.009	0.269	0.326			
AA48653 Early growth response protein 1	AA44602	7 Early growth response 2 (Krox-20 (Drosophila) homolog)							
AA845016 Edg-2	AA48653	3 Early growth response protein 1							
1921 1922 1923 1924 1925		Eag-2 Ea		-0.031	-0.332	-0.027	-0.298	1.535	
AA845015 Elastase 1, pencreatic (elastase IIA) AA845167 ELASTASE IIIA PRECURSOR AA845167 ELASTASE IIIB PRECURSOR M45415 ELASTASE IIIB PRECURSOR T57919 Electron-transfer-flavoprotein, alpha polypeptide (glutaric acidurie II) AA844414 ILK1 member of ETS procepen family -0.044 -0.164 0.322 0.252 -0.233 -0.590			-0.744	-0.309					
AA845167 ELASTASE IIIA PRECURSOR 0.878 0.767 - 0.713 - 2.237 - 1.660 0.025 W45415 ELASTASE IIIB PRECURSOR 0.281 0.545 0.688 1.046 T57919 Electron-transfer-flavoprotein, alpha polypeptide (glutaric acidurie II) 0.044 0.164 0.322 0.252 -0.233 -0.590	AA84501	5 Elastase 1, pancreatic (elastase IIA)							
W45415 ELAST INSE IIIS PRECURSOR T57919 Electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II) -0,108 0.296 0.281 0.545 0.688 1.046 -0,108 0.296 0.281 0.545 0.688 1.046 -0,044 -0,164 0.322 0.252 -0,233 -0,590								0.025	
AA844141 FLK1 member of ETS oncogene family -0.044 -0.104 0.322 0.232 -0.233 -0.335		Electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	-0.108	0.296	0.281	0.545			
H61758 ELK4, ETS-domain protein (SRF accessory protein 1) NOTE: Symbol and name provisional -0.121 0.181 0.267 0.341 0.103 -0.126		1 FLK1 member of ETS oncodene family							
		ELK4, ETS-domain protein (SRF accessory protein 1) NOTE: Symbol and name provisional	-0.121	0.161	0.267	0.341	0.103	-U. 120	

400	Gene Name	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
ACC AA446108	Endoglin (Osler-Rendu-Weber syndrome 1)	2.203	0.860	1.254	2.231	1.594	-1.415	
R20666	Endothelial differentiation protein (edg-1)	-0.311 -0.278	-0.083 -0.261	-0.038 0.303	0.018 0.002	0.083 0.146	1.362 1.536	
H11003 T67004	Endothelin 1 {alternative products} Endothelin 3	0.123	0.258	0.262	0.252	0.075	0.842	
AA279429	Endothelin converting enzyme 1	-0.065 -0.178	-0.270 0.146	-0.225 0.305	-0.261 0.092	-0.243 0.497	-0.116 0.811	
AA450009 H28710	Endothelin receptor type A Endothelin receptor type B	0.425	0.355	0.473	0.440	0.327	1.342	
	Enolase 2, (gamma, neuronal)	0.850	0.287	0.630	0.530	0.877	-0.060	
AA029419	Envoplakin	0.634 1.384	0.204 0.450	0.136 0.803	0.351 0.982	-0.237 1.268	-0.140 -2.822	
R02373	Enyol-coA: hydratase 3-hydroxyacyl-coA dehydrogenase EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1 PRECURSOR	0.430	0.614	0.244	0.209	0.498	-1.100	
W48713	Epidermal growth factor receptor	-0.180	-0.095	0.247 0.016	-0.017 -0.458	0.174 -0.359	-0.641 1.229	
AA490223	Epidermal growth factor receptor pathway substrate 15 Epoxide hydrolase 1, microsomal (xenobiotic)	-0.359 -0.318	-0.194 -0.072	0.112	0.236	0.228	1.420	
R73525	Epoxide hydrolase 1, microsomai (xenobiotic) Epoxide hydrolase 2, cytoplasmic	-0.433	0.268	-0.153	-0.287	-0.467	-0.094	
H27912	ER LUMEN PROTEIN RETAINING RECEPTOR 1	0.127 -0.401	0.387 -0.051	0.171 -0.044	0.097 -0.204	0.693 -0.200	-0.228 0.744	
AA626867	ER LUMEN PROTEIN RETAINING RECEPTOR 2 ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR	-1.006	-0.404	-0.746	-0.322	-0.562	0.629	
	ERGIC-53 PROTEIN PRECURSOR	-0.268	0.237	0.659	0.517	0.072	1.748	
R62817	ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN	0.082 0.837	0.441 0.035	0.176 0.528	0.251 0.029	0.495 0.367	1.783 1.229	
AA449835 N55461	Erythrocyte membrane protein band 4.2 Erythrocyte membrane protein band 4.9 (dematin)	-0.555	-0.355	-0.106	-0.642	-0.320	0.741	
T48950	ERYTHROCYTE PLASMA MEMBRANE 50 KD GLYCOPROTEIN	0.305	0.542	-0.196	-0.211	0.342	-0.258 1.398	
	Erythroid alpha-spectrin	0.325 -0.222	-0.033 0.278	0.521 0.026	-0.012 -0.014	-0.074 0.664	1.524	
H15574 T64482	Erythropoietin receptor Esterase D/formylglutathione hydrolase	0.962	0.131	0.502	0.106	0.082	1.295	
AA291749	Estrogen receptor	-0.855	-0.284	-0.390	-0.739 0.277	0.907 0.881	0.936 1.301	
AA010400	Ets variant gene 4 (E1A enhancer-binding protein, E1AF)	0.444 0.429	0.666 0.390	0.112 0.645	0.349	-0.038	2.204	
AA460265 H81220	ETS-RELATED PROTEIN ERM ETS-RELATED TRANSCRIPTION FACTOR ELF-1	-0.175	0.174	0.076	0.265	0.061	1.995	
N79030	EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34	0.231	0.221	0.363	0.175 0.114	0.707 0.642	1.928 1.963	
AA872402	EUKARYOTIC INITIATION FACTOR 4B	0.221 -0.295	0.440 0.045	0.553 -0.043	0.114	-0.353	-0.028	
AA456664 R43766	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 Eukaryotic translation elongation factor 2	-0.261	0.401	0.058	-0.029	0.579	-0.569	
AA669452	Eukaryotic translation initiation factor 2A	1.166	0.272	0.740 0.053	0.487 0.142	0.622 0.467	0.486 0.825	
H63361	Eukaryotic translation initiation factor 2B (eIF-2B) alpha subunit	-0.150 -0.061	0.254 -0.142	-0.289	-0.631	-0.079	1.886	
N95165	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit Eukaryotic translation initiation factor 4A (eIF-4A) isoform 2	0.107	0.501	0.007	-0.025	0.304	0.352	
AA194246	Eukaryotic translation initiation factor 4E	-0.391	0.264 -0.361	-0.060 0.119	-0.086 -0.331	0.693 -0.180	0.713 0.767	
	Eukaryotic translation initiation factor 5 (eIF5)	-0.041 -0.428	-0.472	-0.802	-0.441	-0.935	0.906	
AA181023 AA411380	EVI2A PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE 2A PROTEIN)	-0.074	-0.247	0.444	-0.110	-0.067	0.871	
AA159620	EVI2B PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE 2B PROTEIN)	-0.077 0.052	0.516 0.328	-0.207 -0.028	-0.074 0.101	-0.337 0.758	1.033 0.953	
R32756	Ewing sarcoma breakpoint region 1 Excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes over	0.480	1.577	0.660	0.179	0.735	1.253	
T95289 R54492	Excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pi	0.621	0.188	0.147	0.242	0.223	1.359	
AA453742	EXCITATORY AMINO ACID TRANSPORTER 1	-0.785 0.963	-0.360 0.593	-1.140 0.345	-0.506 -0.119	-0.005 0.836	-0.001 1.481	
W25105	Exostoses (multiple) 2	0.539	0.606	0.510	0.448	0.185	1.300	
AA487582 AA454819	EXTRACELLULAR SIGNAL-REGULATED KINASE 1	0.525	0.339	-0.047	0.323	0.520	0.734	
AA400982	EXTRACELLULAR SIGNAL-REGULATED KINASE 3	0.527 -0.375	0.496 -0.177	0.038 0.122	0.430 -0.668	0.617 -0.281	0.745 0.912	
AA463924 H62396	FACTOR VIII INTRON 22 PROTEIN Fanconi anemia complementation group C	0.160	-0.016	0.117	0.418	0.509	0.957	
	Forconi anemia, complementation group A	0.684	0.251	0.302	0.269	-0.056	0.502 0.869	
T65790	Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, gen	0.099	0.186 -0.006	0.284 0.299	0.054 -0.150	0.892 -0.117	-0.362	
AA112105	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE Famesyltransferase, CAAX box, alpha	-0.235	-0.210	-0.202	-0.450	-0.628	1.028	
T53220	Fatty acid binding protein 2, intestinal	-0.149 0.048	-0.437 0.341	-0.119 0.048	-0.628 0.246	-0.467 0.280	1.776 0.647	
N92901	Fatty acid binding protein 4, adipocyte	0.048	0.066	0.240	0.196	0.115	0.026	
AA634109	FATTY ACID-BINDING PROTEIN, HEART Fc fragment of IgG, low affinity IIa, receptor for (CD32)	0.217	0.374	0.293	0.550	0.574	0.524	
T64893	Ferrochelatase (protoporphyria)	0.880 -0.088	0.691 -0.177	0.366 0.138	0.206 0.008	0.162 0.556	0.548 0.914	
AA663986	Fibrillarin Fibrillin 1 (Marfan syndrome)	0.791	0.731	0.110	0.179	0.179	0.302	
W58367	Fibrillin 2	0.278	-0.169	0.241	0.939	0.219 -0.333	1.304 2.247	
T74257	FIBRINOGEN BETA CHAIN PRECURSOR	-0.075 0.344	-0.266 0.781	-0.112 0.601	-0.208 0.985	0.152	1.378	
T94279	FIBRINOGEN GAMMA-A CHAIN PRECURSOR Fibrinogen, A alpha polypeptide	-0.343	-0.455	0.285	0.307	-0.410	-0.059	
AA015914	Fibroblast growth factor 1 (acidic)(alternative products)	0.237	0.226	-0.704	-0.062 0.256	-0.763 0.718	0.863 0.899	
W51760	Fibroblast growth factor 2 (basic) Fibroblast growth factor 7 (keratinocyte growth factor)	0.522 -0.302	0.522 0.131	0.127 0.187	0.143	0.446	0.400	
AA443093	Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, cra	-0.021	0.353	0.102	-0.194	-0.050	0.909	
AA419620	Fibrobiast growth factor receptor 3 (achondroplasia, thanatophoric dwarrism)	0.117 0.383	0.275 -0.298	0.340	0.059	0.571 0.052	0.753 0.510	
	Fibroblast growth factor receptor 4 Fibromodulin	0.344	0.279	0.435	0.357	0.247	1.078	
	Fibronectin 1	0.096	0.180	0.017 0.167	-0.535 0.599	-0.393 0.192	1.136 1.339	
AA134871		-0.129 0.023	0.137 0.104	0.167	-0.046	0.182	0.635	
AA452840 AA598978	Filamin 1 (actin-binding protein-280)	0.182	0.158	0.364	0.064	0.262	0.325	
AA625981	FK506-binding protein 1 (12kD)	-0.049 0.283	0.254 0.032	-0.087 0.187	0.149 -0.316	0.725 -0.265	0.494 0.315	
AA482251	FK508-binding protein 3 (25kD) FK508-BINDING PROTEIN PRECURSOR	0.768	0.637	0.824	0.440	1.692	0.020	
R75820 N91952	FKBP-RAPAMYCIN ASSOCIATED PROTEIN	0.003	0.207	-0.051	-0.146	0.543	1.015	
AA620553	FLAP ENDONUCLEASE-1	0.933 -0.959	-0.082 -0.668	0.173 -0.539	-0.169 -0.697	-0.322 -0.280	0.880 0.775	
H52119	Flavin containing monooxygenase 5 Flavin-containing monooxygenase 1	0.205	-0.095	0.272	-0.076	-0.109	0.952	
H71848	Flavin-containing monooxygenase 2	-0.445	0.161	0.094	0.342	0.314	0.819	
N31492	Flavin-containing monooxygenase 4	-0.333 0.124	-0.451 0.285	0.280 -0.105	0.510 0.259	-0.325 0.537	0:552 0:584	
AA521453 T52674	Flightless I (Drosophila) homolog Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	0.041	0.343	0.342	0.072	0.905	0.345	
R24530	Folate receptor 1 (adult)	-0.451	0.036	-0.011	-0.137	0.585 0.063	0.322 0.390	
AA453816	FOLATE RECEPTOR BETA PRECURSOR	0.613 -0.095	-0.081 -1.022	0.055 -0.863	-0.845 -1.180	-0.817	0.555	
W47362 AA458992	FOLATE RECEPTOR GAMMA PRECURSOR Follicular lymphoma variant translocation 1	0.511	0.004	0.287	-0.036	0.907	0.895	
AA425767	Formyl peptide receptor 1	-0.112	0.097 -0.306	0.383 -0.447	-0.236 -0.700	0.579 0.113	0.889 0.982	
R79948	Formyl peptide receptor-like 1 FOS-RELATED ANTIGEN 1	-1.036 -0.682	-0.306	-0.447	-0.700	-0.483	0.424	
H96643 T58873	FOS-RELATED ANTIGEN 2	0.584	1.086	0.608	0.857	0.596	0.696	
AA256123	Fragile histidine triad gene product	-0.757 -0.279	-0.322 0.092	-0.616 0.142	-0.356 -0.366	-0.143 0.670	-0.496 0.075	
N48355 AA253413	Fragile X mental retardation 1 Friedreich ataxia	-0.044	0.133	0.248	-0.202	0.487	0.473	
N50806	Friend leukemia virus integration 1	-0.207	0.166	0.099 0.148	0.037 -0.249	0.360 0.077	0.488 0.504	
	Fructose-bisphosphatase 1	-0.127 -0.940	0.136 -0.876	-0.714	-1.301	-0.411	0.477	
N95761 R25419	Fucosidase, alpha-L- 1, tissue Fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	0.587	0.444	0.557	0.425	0.421	0.842	
	Fumarate hydratase	0.615	0.351	0.175	0.439	0.131	0.956	

ACC	Gene Name	ZR75	YY3	YY1	468	MPI	231	(log base 2 rai
W94120	Fumarylacetoacetate	-0.066	-0.776	0.084	0.325	-0.439	0.692	
N66144	FYN oncogene related to SRC, FGR, YES	0.541	0.753	-0.112	0.131	0.268	0.095	
AA201284	G protein-coupled receptor kinase 6	-0.166	-0.342	0.083	-0.126	-0.437	0.246	
N23898	G PROTEIN-COUPLED RECEPTOR KINASE GRK4	-0.151	-0.078	0.336	-0.126	0.859	0.245	
N23090	G PROTEIN-COUPLED RECEPTOR KINASE GRK5	-0.844	-0.767	-1.260	-0.286	-1.256	-0.204	
		1.467	0.502	1.413	0.936	0.787	0.311	
AA454696	G1 to S phase transition 1	0.664	0.645	0.644	-0.363	-0.158	0.527	
	G1/S-SPECIFIC CYCLIN C GA-binding protein transcription factor, alpha subunit (60kD)	0.456	0.478	0.129	0.378	0.304	0.450	
H96241	GA-binding protein transcription factor, alpita subunit (conc)	0.451	0.425	0.174	0.462	0.219	0.282	
H91651	GA-binding protein transcription factor, beta subunit 2 (47kD)	-0.089	0.145	0.294	0.219	-0.092	0.415	
AA857212	Galactose-1-phosphate undyl transferase	-0.376	0.119	-0.218	-0.583	0.518	0.996	
	Galactosidase, beta 1	0.012	-0.453	0.213	-0.161	-0.148	0.817	
	GALECTIN-2	-0.500	0.045	0.158	0.454	-0.014	0.709	
AA780079	GAMMA CRYSTALLIN A		0.197	0.599	0.227	0.120	0.363	
T60048	Gamma-actin, enteric smooth muscle form	0.347			-0.150	0.657	0.669	
R38700	Gamma-aminobutyric acid (GABA) A receptor, alpha 6	0.503	0.848	0.151			0.867	
R45230	Gamma-aminobutyric acid (GABA) A receptor, beta 1	0.036	0.467	-0.059	0.199	0.908		
R40790	Gamma-aminobutyric acid (GABA) A receptor, gamma 2	-0.228	0.215	-0.258	-0.609	0.251	0.551	
R15435	Gamma-aminobutyric acidA receptor alpha 2 subunit [human, fetal brain, mRNA, 2189 nt]	-1.128	-0.660	-1.124	-1.476	-0.069	0.628	
AA150687	GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR	0.078	-0.248	-0.712	-0.389	-0.465	0.695	
AA630800	GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR	-0.054	0.045	0.093	1.480	0.148	0.895	
AA453471	GANGLIOSIDE GM2 ACTIVATOR PRECURSOR	0.170	0.497	-0.298	-0.168	0.036	0.864	
H44032	Gap junction protein, alpha 4, 37kD (connexin 37)	1.198	0.172	0.768	0.777	2.632	1.089	
N62394	Gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)	-0.566	-0.713	-0.246	-1.192	-0.803	0.689	
	Gap junction protein, beta 2, 26kD (connexin 26)	0.110	0.613	0.190	0.136	0.846	0.954	
AA256172	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	0.017	0.477	0.165	0.210	0.838	0.430	
	Gastrin-releasing peptide	-0.217	0.296	0.133	-0.115	-0.114	0.487	
R06446	GATA-binding protein 1 (globin transcription factor 1)	0.377	0.155	0.331	0.653	0.293	0.650	
		0.509	0.025	0.212	0.451	-0.005	0.850	
H72875	GATA-binding protein 3	-0.198	0.081	-0.065	-0.309	-0.067	0.743	
H94857	GCN5-like 1	-0.341	0.223	0.216	0.080	-0.240	0.851	
	GC-RICH SEQUENCE DNA-BINDING FACTOR GELSOLIN PRECURSOR, PLASMA	-0.296	0.787	-0.057	0.505	0.315	0.864	
H72028	GELSOLIN PRECURSOR, FLASHIA	0.117	0.644	0.196	0.219	0.919	0.836	
H23978	General transcription factor IIB	1.598	0.287	0.749	0.308	1.000	0.922	
AA282092	General transcription factor IIF, polypeptide 1 (74kD subunit)	0.232	0.116	0.124	0.015	0.684	1.145	
AA456147	General transcription factor IIIA	-0.182	0.269	0.126	-0.168	0.393	0.862	
AA133566	General transcription factor TFIIE beta subunit, 34 kD		-0.093	0.395	-0.295	0.695	0.424	
AA853954	Germ cell nuclear factor [human, embryonal carcinoma NT2/D1, mRNA, 1916 nt]	-0.051					-0.439	
AA418036	GLI3 PROTEIN	0.528	0.485	0.480	0.269	0.400		
H22653	GLIA MATURATION FACTOR BETA	0.605	0.582	0.291	0.109	0.712	0.765	
	Gliat fibrillary acidic protein	-0.281	-0.298	-0.092	-0.475	0.077	0.701	
R09069	Glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen st	0.251	0.888	0.415	0.064	1.059	0.770	
	Glucocorticoid receptor	-0.178	0.359	-0.087	0.038	0.579	0.544	
	Glucocorticoid receptor alpha {alternative products}	-0.098	0.095	-0.015	0.058	0.525	0.557	
N66871		-0.524	-0.132	-0.193	-0.147	-0.129	0.913	
T67006	Glucokinase regulator Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	2.439	-0.033	2.671	1.246	1.801	0.956	
		0.098	-0.509	-0.018	-0.318	-0.281	0.836	
AA401111	Glucose phosphate isomerase	0.365	0.781	0.204	0.215	0.746	0.807	
	GLUCOSE TRANSPORTER TYPE 3, BRAIN	-0.460	-0.427	-0.484	-0.613	-0.121	0.988	
T98887	Glucose-6-phosphatase	0.085	0.207	-0.001	0.052	0.137	0.803	
	Glucose-6-phosphate dehydrogenase	0.296	-0.468	-0.488	-0.442	-0.350	0.863	
AA424938	Glucose-8-phosphate dehydrogenase	0.179	0.284	0.321	0.053	-0.005	0.860	
N34827	Glucuronidase, beta	0.480	0.360	0.257	0.400	1.043	0.543	
AA018457	Glutamate decarboxylase 1 (brain, 67kD)		0.300	0.349	0.083	0.459	-0.060	
R44005	Glutamate decarboxylase 2	0.360		-0.075	0.035	0.512	0.465	
H23267	GLUTAMATE RECEPTOR 1 PRECURSOR	0.239	0.493		-0.401	0.730	0.562	
R36886	GLUTAMATE RECEPTOR 3 PRECURSOR	0.408	0.562	0.137		1.323	0.721	
H28734	Glutamate receptor, ionotropic, AMPA 2	0.263	0.705	0.649	0.336		1.074	
AA058857	Glutamate receptor, ionotropic, kainate 5	0.510	0.526	0.290	0.290	0.715		
R88267	Glutamate receptor, ionotropic, N-methyl D-aspartate 1	0.155	0.312	0.262	0.584	0.424	1.259	
AA670430	Glutamate receptor, metabotropic 3	-0.816	-0.565	-0.915	-0.783	-1.025	1.054	
W96179	Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)	0.564	0.615	0.409	0.288	0.808	1.260	
H56069	GLUTAMATE-CYSTEINE LIGASE CATALYTIC SUBUNIT	1.316	1.462	0.800	0.904	0.861	1.036	
H22856	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	-0.770	-0.293	-1.237	-0.890	-0.937	0.862	
AA487521	Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	0.264	-0.133	0.260	0.598	-0.026	1.053	
A A 470E71	Glutamine-fructose-6-phosphate transaminase	0.259	0.284	-0.057	0.021	0.345	0.941	
	GLUTAMINYL-TRNA SYNTHETASE	0.052	0.103	0.188	1.526	0.243	-0.794	
	Glutamyl aminopeptidase (aminopeptidase A)	-0.581	-0.242	-0.480	-0.706	-0.330	0.449	
		-0.091	0.140	-0.429	-0.006	-0.226	0.769	
	Glutaredoxin (thioltransferase)	-0.579	-0.780	-0.392	-0.934	-0.447	0.675	
R56638	Glutaryl-Coenzyme A dehydrogenase	0.294	0.147	0.508	0.160	0.916	0.804	
	Glutathione peroxidase 1	-0.441	0.377	-0.227	0.099	0.494	0.752	
	Glutathione peroxidase 2, gastrointestinal	-0.777	-0.550	-0.410	-0.846	-0.589	0.862	·
	Glutathione peroxidase 3 (plasma)	0.461	0.246	-0.132	-0.006	0.593	0.914	
	Glutathione reductase	0.591	0.255	0.443	0.752	0.435	0.999	
T73468	Glutathione S-transferase A2	-0.481	-0.449	-0.227	-0.413	0.037	0.988	
N30096	Glutathione S-transferase A3		1.044	0.377	0.220	0.467	0.817	
	Glutathione S-transferase M2 (muscle)	0.582		1.286	0.668	1.002	0.277	
R63065	Glutathione S-transferase M3 (brain)	1.295	1.598 0.161	0.026	-0.124	0.059	0.373	
	Glutathione S-transferase M4	-0.062		0.026	-0.124	0.499	0.702	
	Glutathione S-transferase M4	-0.500	-0.099				0.060	
	Glutathione S-transferase M5	0.647	0.630	0.141	0.393	0.752		
H99813	Glutathione S-transferase theta 1	-0.493	-0.438	-0.350	-0.073	-0.035	0.845	
AA490208	Giutathione S-transferase theta 2	0.675	0.582	0.206	0.173	0.774	0.873	
AA495936	GLUTATHIONE S-TRANSFERASE, MICROSOMAL	0.366	0.480	0.250	0.123	0.812	1.011	
	Glutathione synthetase	0.504	0.487	0.408	0.013	1.126	0.908	
R33642	Glutathione-S-transferase pi-1	-0.297	-0.321	0.083	0.280	-0.073	0.919	
AA405987	Giveerol kinase 2 (testis specific)	0.104	0.099	0.558	0.248	0.848	0.580	
AA005240	Givcerol-3-phosphate dehydrogenase 2 (mitochondrial)	0.006	-0.079	-0.311	-0.088	0.310	0.569	
R28294	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR	-0.534	800.0	-0.027	-0.231	0.238	0.659	
	Glycine cleavage system protein P (glycine decarboxylase)	-0.010	-0.176	0.290	0.269	-0.201	1.039	
N58494	Glycine cleavage system protein F (glycine decanockylase) Glycine cleavage system protein T (aminomethyltransferase)	2.518	0.502	1.388	2.046	1.080	1.055	
N59532	Glycogen phosphorylase B (brain form)	0.118	0.621	0.254	0.090	-0.026	0.517	
AA40000	C CLYCOCEN PHOSPHORYLASE MUSCLE FORM	-0.169	-0.230	0.210	1.054	-0.412	0.688	
	2 GLYCOGEN PHOSPHORYLASE, MUSCLE FORM	0.426	0.391	0.282	0.107	0.589	0.780	
N52282	Glycogen synthase [human, liver, mRNA, 2912 nt]	0.129	-0.048	0.382	0.226	0.135	0.873	
H08732	Glycogen synthase 1 (muscle)	-0.722	-0.590	-0.444	-0.724	-0.267	0.879	
N70285	Glycophorin A	0.019	-0.005	0.176	0.008	0.251	0.691	
	3 Glycophorin B				0.793	0.582	0.218	
N77392	Glycophorin C	0.179	0.376	0.471			0.218	
T50527	Glycophorin E	-0.146	0.316	-0.002	0.022	0.037		
AA67740	3 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR	0.661	-0.009	0.470	0.779	0.065	0.173	
N92319	Glycoprotein Ib (platelet), beta polypeptide	-0.263	-0.033	-0.191	-0.095	-0.015	0.385	
AA47658	GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE	0.295	0.976	1.130	0.698	1.125	0.580	
	9 Glycyl-tRNA synthetase	-0.880	-0.377	-0.406	-0.638	-0.045	0.798	
	6 Glypican 1	0.176	0.102	-0.148	-0.216	0.697	0.231	
AA04000	6 Gonadotropin-releasing hormone (leutinizing-releasing hormone)	-0.496	-0.051	0.063	0.069	0.512	0.344	
		-0.176	0.122	0.114	0.150	0.095	0.485	
R44739	GRANCALCIN	-0.082	-0.035	0.267	-0.181	0.003	0.764	
	2 Granulin Granulocyte colony-stimulating factor induced gene [human, CML patient, bone marrow mononuclear c	0.332	0.325	0.161	0.209	0.385	0.958	
T57859		0.156	0.630	0.151	0.386	0.285	1.057	
AA28300	7 GRANZYME A PRECURSOR	5.100	2.200	.				

ACC	Gene Name	ZR75 -0.426	YY3 0.037	-0.044	468 0.145	MPI 0.512	231 0.455	(log base 2 ratio
AA478543	Granzyme K (serine protease, granzyme 3) GRAVIN	0.020	0.059	-0.005	0.053	0.219	1.005	
AA485646	G-rich RNA sequence binding factor 1	-0.916	-0.379 -0.017	-0.617 -0.394	-0.980 -0.245	-0.559 0.131	0.747 0.647	
W46900 R89567	GRO1 oncogene (melanoma growth stimulating activity, alpha) Group-specific component (vitamin D binding protein)	0.032	0.387	0.060	0.015	0.739	0.577	
	Growth arrest-specific 1	0.259	0.435	-0.039	0.262	0.659 0.742	0.742 0.242	
H05445	Growth associated protein 43 Growth factor receptor-bound protein 2	0.563 -0.069	0.814 0.173	0.353 0.225	-0.152 0.198	0.949	-0.759	
	Growth hormone receptor	0.441	0.313	0.399	0.838	0.036	0.096	
AA278698	GS1 PROTEIN	0.315 0.319	0.219 0.104	0.227	0.121 0.178	0.314 0.329	0.582 0.719	
	GTP cyclohydrolase 1 (dopa-responsive dystonia) {alternative products} GTPase-activating protein ras p21 (RASA)	0.351	0.590	0.225	0.186	0.883	0.909	
H92232	Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	0.290	0.261	0.143	0.208 -0.127	0.216 0.151	1.166 1.008	
T99303	Guanine nucleotide binding protein (G protein), alpha 15 (Gq class) Guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	-0.425 0.641	-0.291 0.638	-0.120 -0.025	-0.127	0.490	0.821	
H49592 AA406364	Guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	0.830	0.501	0.100	-0.482	0.639	0.774	
AA071330	Guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	-0.235 0.308	0.108 -0.326	0.196 0.081	0.467 -0.845	0.352 -0.235	0.583 -0.356	
AA112660 W92431	Guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1 Guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1	0.050	0.238	0.212	0.279	0.316	-0.113	
R56046	Guanine nucleotide binding protein (G protein), alpha z polypeptide	0.090	0.401	0.246	0.082 0.337	0.901 0.542	-0.608 -0.274	
	Guanine nucleotide binding protein (G protein), beta polypeptide 1 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3	0.861 -0.166	0.697 -0.035	-0.183	0.101	0.270	0.258	
R96220 AA486850	Guanylate binding protein 1, interferon-inducible, 67kD	0.909	0.935	0.515	0.239	0.461	0.563	
W21127	Guanylate cyclase 1, soluble, alpha 2	0.330 0.133	0.349 0.750	0.094 0.616	-0.057 0.684	0.594 0.261	0.654 0.649	
	GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN H factor (complement)-like 1	0.483	0.415	-0.071	0.190	0.677	0.671	
AA133212	H. sapiens cDNA for RFG	-0.204	0.156	0.134 0.069	0.094 0.221	-0.047 -0.153	0.880 0.674	
	H. sapiens RNA for CLCN3 H.sapiens 40 kDa protein kinase related to rat ERK2	0.164 -0.764	0.836 0.363	-0.941	0.190	0.112	0.443	
	H.sapiens 5T4 gene for 5T4 Oncofetal antigen	0.054	0.648	-0.104	-0.210	0.013	0.126	
AA625628	H.sapiens 6C6-Ag mRNA	0.438 0.410	0.075 0.577	-0.232 -0.091	0.291 0.056	0.374 0.364	-0.643 0.999	
AA664241 N70349	H.sapiens ART4 gene	-0.203	-0.019	-0.242	-0.227	0.058	-0.181	
AA028921	H.sapiens beta glucuronidase pseudogene	0.246	0.073	1.168	-0.227 -0.097	0.179 0.388	-0.203 0.729	
	H.sapiens cl.1042 mRNA of DEAD box protein family	0.496 0.273	0.504 0.704	0.350 0.321	0.711	0.125	0.583	
T50096	H.sapiens DAP-1 mRNA H.sapiens DAP-3 mRNA	0.389	0.439	-0.090	-0.161	0.108	0.710	
AA025275	H.sapiens DAP-kinase mRNA	1.128 0.186	0.363 0.184	1.634 0.180	1.036 -0.148	1.271 0.325	0.716 0.576	
AA633811 R77251	H.sapiens E-MAP-115 mRNA	0.299	0.178	0.077	-0.261	0.697	0.601	
AA775410	H.sapiens EMX1 mRNA	-0.067	-0.101 -0.671	0.441 0.149	0.799 -0.210	-0.026 0.083	0.819 -0.646	
	H.sapiens encoding CLA-1 mRNA H.sapiens endonuclease G (ENDOG) mRNA	-0.059 -0.215	-0.512	-0.244	0.113	0.055	-0.168	
	H.sapiens ERC-55 mRNA	0.383	0.757	0.404	0.923	0.074	0.528	
AA424743	H.sapiens ERF-1 mRNA 3' end	0.639	0.685 0.477	0.632 0.407	0.201 0.013	1.211 0.724	0.390	
H17504	H.sapiens ERK3 mRNA H.sapiens garp gene mRNA, complete CDS	-0.196	0.051	-0.066	-0.171	0.349	0.605	
H70775	H.sapiens H2B/I gene	0.216	0.630	0.081	-0.231 0.186	1.081 -0.025	0.415 0.055	
	H.sapiens H4/g gene for H4 histone	-0.354 0.103	-0.150 0.642	-0.025 0.610	0.541	0.589	-0.381	
R44020 AA481026	H.sapiens HBF-1 mRNA for transcription factor H.sapiens hbrm mRNA	0.097	0.204	-0.088	-0.297	0.091	0.154	
AA054321	H.sapiens HCG I mRNA	0.021 -0.460	0.234 -0.109	0.058 -1.040	0.094 0.139	0.519 -0.237	0.361 0.617	
AA485347	H.sapiens HCG V mRNA H.sapiens HE4 mRNA for extracellular proteinase inhibitor homologue	-0.252	-0.935	-0.449	-0.049	0.118	0.369	
AA456088	H.sapiens HEK2 mRNA for protein tyrosine kinase receptor	1.233	0.399	0.162	0.403 0.082	0.536 0.236	0.473 0.663	
N50636	H.sapiens hGDS mRNA for smg GDS	0.247 -0.125	0.180 0.070	0.092 0.460	0.124	0.328	0.546	
AA431440 AA007444	H.sapiens hnRNP-E2 mRNA H.sapiens homeobox protein (HOX-11) mRNA, complete cds	1.436	0.935	1.006	0.698	1.009	0.734	
R44870	H.sapiens HPBRII-4 mRNA	0.828 1.071	0.444 1.854	0.041 0.063	0.121 1.167	0.437 0.360	0.901 0.969	
R51209	H.sapiens hPTPA mRNA H.sapiens Humig mRNA	0.811	0.644	0.451	0.630	0.592	-0.289	
T91261	H.sapiens HUMM9 mRNA	1.214	1.430 0.031	0.806 -0.031	0.556 -0.244	1.069 -0.213	-0.460 -0.110	
	H.sapiens IAI.3B mRNA H.sapiens IL-13Ra mRNA	0.028 0.105	-0.003	-0.522	-0.059	-0.028	0.104	
N50544	H sapiens irlB mRNA	0.742	0.795	-0.146	0.199 -0.634	0.244 -0.048	0.527 -0.274	
T61256	H.sapiens KHK mRNA for ketohexokinase, clone pHKHK3a	-0.551 0.275	0.701 0.038	0.435 0.222	0.147	0.182	0.482	
AA453015 AA504455	H.sapiens LDLC mRNA H.sapiens LDLC mRNA	-0.026	-0.056	-0.007	-0.123	-0.190	0.527	
AA158991	H.sapiens frp mRNA	0.071 0.300	0.267 0.284	0.327 -0.058	0.470 -0.104	0.311 0.434	0.592 1.071	
AA463926	H.sapiens LU gene for Lutheran blood group glycoprotein H.sapiens MADER mRNA	0.634	1.011	0.072	0.087	0.351	0.934	
AA598826	H.sapiens MLN62 mRNA	0.294	0.352	0.123	0.444	0.367	0.751 0.513	
R59212	H.sapiens MN1 mRNA H.sapiens mRNA (clone C-2k) mRNA for serine/threonine protein kinase	1.720 -0.415	1.792 0.005	0.768 0.398	0.162	-0.058	-0.250	
H45967 AA865729	H.sapiens mRNA (coular albinism type 1 related)	0.280	0.430	0.141	0.264	0.571	0.141	
AA447742	H.sapiens mRNA dynein-related protein	0.368 0.636	0.158 1.247	0.126 -0.165	-0.118 -0.256	0.432 0.416	0.426 1.005	
AA670155	H.sapiens mRNA encoding GPI-anchored protein p137 H.sapiens mRNA for -14 gene, containing globin regulatory element	0.336	0.402	0.421	0.732	0.290	0.056	
AA487914	H.sapiens mRNA for 17-beta-hydroxysteroid dehydrogenase	0.229	0.209	0.310	0.496 1.135	0.370 0.447	-0.007 0.383	
R87497	H.sapiens mRNA for 2.19 gene	-0.328 0.048	-0.441 0.363	0.757 -0.688	0.152	-0.294	0.935	
N34372 AA454852	H.sapiens mRNA for 218kD Mi-2 protein H.sapiens mRNA for 55.11 binding protein	0.111	0.035	0.502	0.552	0.864	1.041	
AA598861	H.sapiens mRNA for a cell surface protein	-0.851 -0.381	-0.358 -0.369	-0.434 -0.122	-0.411 0.168	0.044 -0.360	1.062 0.911	
R68237 N49204	H.sapiens mRNA for activin type It receptor H.sapiens mRNA for acylphosphatase, muscle type (MT) isoenzyme	0.783	0.708	0.603	0.620	0.954	0.886	,
	H.sapiens mRNA for adaptor protein p150	0.445	0.367	-0.122	0.235	-0.280	0.175	
AA700054	H.sapiens mRNA for adipophilin	0.601 0.126	-1.172 0.122	0.796 0.597	-0.975 1.440	-0.573 0.106	0.286	
T54462 H11808	H.sapiens mRNA for AFX protein H.sapiens mRNA for AICL (activation-induced C-type lectin)	-0.028	0.419	0.169	0.177	0.152	0.092	
AA609609	H.sapiens mRNA for alkB protein homolog	-0.224	-0.056 0.166	-0.432 0.691	-0.335 0.237	-0.231 0.374	0.025 0.170	
AA463498	H.sapiens mRNA for alpha 4 protein H.sapiens mRNA for alpha endosulfine	0.367 0.281	0.166	0.286	0.224	0.649	0.716	
R40850	H.sapiens mRNA for alpha-centractin	0.280	0.267	-0.201	0.177 -0.095	0.146 0.153	0.806 0.591	
R40850	H.sapiens mRNA for alpha-centractin	0.477 -0.223	0.525 -0.040	0.157 0.134	-0.095 0.445	0.153	1.012	
R32450 AA453477	H.sapiens mRNA for aminopeptidase H.sapiens mRNA for aminopeptidase P-like	0.036	-0.212	-0.055	-0.299	0.002	1.007	
AA018906	H.sapiens mRNA for AP-2 beta transcription factor	0.156	0.359 -0.642	0.986 -0.421	1.615 -0.539	0.141 -1.000	0.187 0.390	
N95381	H.sapiens mRNA for apoptosis specific protein H.sapiens mRNA for Arg protein tyrosine kinase-binding protein	-0.630 0.229	0.156	-0.421	0.014	0.117	0.420	
N21334 AA778346	H.sapiens mRNA for arginine methyltransferase	0.757	0.677	0.562	0.715	0.791	-0.194	
AA676836	H.sapiens mRNA for ASM-like phosphodiesterase 3a	0.409 0.151	0.568 0.434	-0.005 0.386	1.063 0.606	0.320 0.779	-0.188 0.238	
H92234	H.sapiens mRNA for axonal transporter of synaptic vesicles H.sapiens mRNA for basic transcription factor 2, 34 kD subunit	0.562	1.519	0.615	0.431	0.630	0.302	
AA598868	H.sapiens mRNA for beta-COP	0.602 -0.196	0.482 0.189	0.415 0.325	0.298 0.031	0.338 -0.023	0.545 0.905	
AA171449	H.sapiens mRNA for biphenyl hydrolase-related protein H.sapiens mRNA for bleomycin hydrolase	-0.196	-0.207	0.548	0.739	-0.014	0.670	
AA41/68	1 11,00 piono ministra no montry di riyano acco							

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ACC Gene Name	ZR75	YY3	YY1 0.232	468 1.469	MPI 0.198	231 0.416	(log base 2 ratio
AA683058 H.sapiens mRNA for BS69 protein	0.232 0.438	0.371 0.577	1.101	1.859	0.263	0.483	
N22178 H.sapiens mRNA for C1D protein AA420997 H.sapiens mRNA for calicin (partial)	0.203	0.158	0.366	-0.132	0.639	0.506	
N72193 H.sapiens mRNA for caltractin	-0.047	0.375	-0.011	-0.215	0.511	0.904 0.155	
R91503 H.sapiens mRNA for canalicular multidrug resistance protein	0.454 -0.172	0.720 0.378	0.353 0.030	0.480 0.034	-0.101 0.005	-0.478	
AA046523 H.sapiens mRNA for centrin gene AA404280 H.sapiens mRNA for CHD5 protein	0.358	0.085	0.285	0.319	0.523	-0.720	
W58658 H.sapiens mRNA for CLPP	0.486	0.607	1.325	3.090	0.014	0.264	
AA082943 H.sapiens mRNA for cyclin G1	-0.552 -0.162	0.077 -0.337	-0.060 -0.227	-0.355 -0.748	0.215 -0.226	-0.506 0.102	
AA488072 H.sapiens mRNA for cytokine inducible nuclear protein	-0.024	-0.080	-0.077	0.150	0.005	0.676	
AA422058 H.sapiens mRNA for D1075-like gene AA033564 H.sapiens mRNA for DGCR6 protein	0.491	0.135	-0.358	-0.043	-0.358	0.262	
AA043347 H.sapiens mRNA for disintegrin-metalloprotease (partial)	0.504	0.274	0.098	0.304	0.309 0.407	0.546 0.548	
N33920 H.sapiens mRNA for diubiquitin	-0.086 -0.342	0.396 0.185	-0.001 0.154	0.266 0.518	0.212	0.738	
H09055 H.sapiens mRNA for DNA (cytosin-5)-methyltransferase H09055 H.sapiens mRNA for DNA (cytosin-5)-methyltransferase	0.269	0.468	0.037	0.019	-0.022	0.894	
R54359 H.sapiens mRNA for DNA ligase IV	-0.079	0.028	0.321	0.132	0.054	0.278	
N40945 H.sapiens mRNA for DRES9 protein	0.605	0.534	0.782	0.839 -0.172	0.846 0.650	0.317 1.309	
AA488168 H.sapiens mRNA for dynactin	0.215 -0.124	0.416 -0.009	0.296	-0.172	0.370	-0.164	
H97778 H.sapiens mRNA for E-cadherin R43973 H.sapiens mRNA for elongation factor-1-gamma	-0.057	-0.127	0.191	0.149	-0.054	0.343	
R43973 H.sapiens mRNA for elongation factor-1-gamma R43973 H.sapiens mRNA for elongation factor-1-gamma	0.318	0.205	0.047	-0.275	0.229	0.078	
R45183 H.sapiens mRNA for elongations factor Tu-mitochondrial	-0.358	0.569 1.454	0.689 -0.847	-0.362 -0.364	-0.715 -0.676	0.564 0.611	
R45183 H. sapiens mRNA for elongations factor Tu-mitochondrial	-0.523 0.712	0.615	-0.002	0.337	0.344	0.347	
W46577 H.sapiens mRNA for ESM-1 protein AA167223 H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus	0.405	0.883	0.366	0.416	0.290	0.705	
W93092 H.sapiens mRNA for FAN protein	0.760	0.978	0.444	0.750	0.273	0.998	
W72310 H.sapiens mRNA for FAST kinase	0.184	0.546 -0.042	0.272 -0.731	0.142 -0.105	0.642 -0.522	0.257 0.435	
H56349 H.sapiens mRNA for fibrinogen-like protein (pT49 protein)	-0.377 -0.087	0.132	0.069	-0.234	0.475	0.490	
AA709158 H.sapiens mRNA for G13 protein AA434117 H.sapiens mRNA for G9a	-0.177	0.204	-0.153	0.227	0.430	0.935	
AA453813 H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase	0.021	0.361	0.209	0.242	0.173	0.704	
N78621 H.sapiens mRNA for gamma-adaptin	0.364 0.167	0.631 0.438	-0.263 1.028	-0.088 0.323	-0.136 0.401	0.435 0.768	
R55620 H.sapiens mRNA for GicNac-1-P transferase	0.800	0.629	0.560	0.486	0.409	0.662	
AA282134 H.sapiens mRNA for glutamine cyclotransferase AA411679 H.sapiens mRNA for glycogenin	0.126	0.682	0.570	0.374	0.350	0.787	
AA489314 H.sapiens mRNA for gp25L2 protein	0.891	0.672	1.020	0.579	0.342 0.121	1.021 0.246	
N70544 H.sapiens mRNA for GPI8 protein	-0.126 -0.245	0.446 0.104	-0.106 0.235	0.357 0.125	0.121	0.214	
AA456291 H.sapiens mRNA for GTP-binding protein AA701554 H.sapiens mRNA for hogVill protein	0.349	0.338	0.727	1.010	0.192	0.494	
AA701554 H.sapiens mRNA for HE3(alpha)	-0.321	-0.180	-0.080	-0.223	0.159	0.681	
H18950 H.sapiens mRNA for hepatocyte nuclear factor 4 gamma	-0.198	0.129	0.646 0.191	-0.090 0.198	-0.006 0.339	0.677 0.686	
AA064638 H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)	-0.221 -0.407	0.274 0.409	-0.591	-0.729	-0.314	0.610	
AA034250 H.sapiens mRNA for HES1 protein AA490471 H.sapiens mRNA for high endothelial venule	0.774	0.338	0.547	0.157	0.326	0.722	
T40541 H saniens mRNA for human giant larvae homolog	0.165	0.182	0.241	0.579	-0.050	0.790	
AA035310 H.sapiens mRNA for hypothetical protein downstream of DMPK and DMAHP	0.068	0.037	0.275 -0.081	1.009 0.161	0.030 -0.378	0.977 1.357	
T52362 H.sapiens mRNA for IcIn protein	0.549 -0.853	0.804 -0.352	-0.623	-0.860	-0.689	0.826	
R52796 H.sapiens mRNA for IL13 receptor R51362 H.sapiens mRNA for imagen 38	-1.281	-0.978	-1.306	-0.931	-1.047	1.050	
R51362 H.sapiens mRNA for imogen 38 T58773 H.sapiens mRNA for InsP3 5-phosphatase	0.113	0.164	-0.077	-0.391	-0.790	0.712	
H68922 H.sapiens mRNA for integrin, alpha subunit	0.164	0.122 0.902	0.400 0.234	0.225 0.459	0.331 0.033	1.068 0.391	
T67884 H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3	0.623 -0.095	-0.303	0.504	0.210	0.000	0.709	
AA456570 H.sapiens mRNA for interferon regulatory factor 3 AA455272 H.sapiens mRNA for ITBA1 protein	-0.488	-0.081	-0.179	-0.198	-0.218	0.343	
AA479062 H.sapiens mRNA for ITBA2 protein	0.618	0.580	0.077	0.407	-0.337	-0.561 0.025	
AA774230 H.sapiens mRNA for ITBA4 gene	0.171 0.252	0.092	0.170 0.554	1.082 -0.334	-0.179 0.065	-0.657	
AA454947 H.sapiens mRNA for kinase A anchor protein T65407 H.sapiens mRNA for L-3-hydroxyacyl-CoA dehydrogenase	0.103	0.491	0.409	0.086	-0.023	0.660	
T65407 H.sapiens mRNA for L-3-hydroxyacyi-CoA denydrogenase AA677534 H.sapiens mRNA for laminin	0.075	0.240	0.615	0.837	-0.044	0.947	
AA775091 H.sapiens mRNA for leucine zipper protein	-0.043 0.382	-0.112 0.747	-0.099 -0.086	-0.208 0.208	-0.154 0.035	0.892 1.502	
AA088861 H.sapiens mRNA for LI-cadherin	-0.202	0.094	-0.260	0.520	0.051	0.718	
AA630320 H.sapiens mRNA for Lon protease-like protein AA504113 H.sapiens mRNA for M phase phosphoprotein 10	-0.099	0.076	0.064	-0.171	0.277	0.580	
AA401693 H.sapiens mRNA for M130 antigen	1.367	0.878	0.477 0.278	1.876 0.165	0.557 0.429	0.902 0.375	
AA448468 H.sapiens mRNA for MACH-alpha-2 protein	0.033 -0.339	0.277 -0.216	-0.151	0.111	-0.196	-0.331	
AA455056 H.sapiens mRNA for MAP kinase activated protein kinase AA126009 H.sapiens mRNA for MAT8 protein	-1.848	-0.843	-0.837	-0.688	-0.800	-0.328	
AA433944 H.sapiens mRNA for mediator of receptor-induced toxicity	0.060	0.341	0.488	0.165 0.041	0.718 -0.289	0.639 0.653	
R53541 H.sapiens mRNA for melanoma-associated chondroitin sulfate proteoglycan (MCSP)	0.186 -0.352	-0.181 -0.215	0.233 0.361	0.107	0.071	0.750	
N33214 H.sapiens mRNA for membrane-type matrix metalloproteinase 1 H77597 H.sapiens mRNA for metallothionein	0.582	0.124	-0.674	-0.441	-0.018	0.331	
H77597 H.sapiens mRNA for metallothionein AA281347 H.sapiens mRNA for MHC class i promoter binding protein	0.196	0.693	0.491	0.300	0.708	-0.095	
AA609976 H.sapiens mRNA for mitochondrial capsule selenoprotein	0.060	0.415	-0.184 0.146	0.266 0.230	0.362 0.191	0.338 -0.447	
H25223 H.sapiens mRNA for Mox-2 N29844 H.sapiens mRNA for M-phase phosphoprotein, mpp11	0.479 -0.374	0.540 -0.315	-0.402	0.230	-0.401	-0.199	
N29844 H.sapiens mRNA for M-phase phosphoprotein, mpp11 AA706968 H.sapiens mRNA for M-phase phosphoprotein, mpp5	0.353	0.432	0.058	0.185	-0.161	0.256	
AA478525 H.sapiens mRNA for M-phase phosphoprotein, mpp6	-0.087	0.168	0.191	0.004 -0.368	0.241 -0.376	-0.293 0.506	
W70051 H.sapiens mRNA for M-phase phosphoprotein, mpp9	-0.086 0.223	-0.218 0.518	0.075 0.455	0.296	0.591	0.686	
AA421701 H.sapiens mRNA for MUF1 protein AA487215 H.sapiens mRNA for myosin light chain kinase	0.289	0.668	-0.056	0.242	0.081	0.651	
AA485871 H.sapiens mRNA for myosin-I beta	0.011	0.533	-0.477	0.060	0.124	0.834	
AA111999 H.sapiens mRNA for NADH dehydrogenase	0.413	0.546	-0.173 0.103	0.471 0.037	-0.117 0.379	-0.013 0.150	
AA779401 H.sapiens mRNA for NADP+-dependent malic enzyme	0.417 -0.088	0.650 0.028	0.093	-0.352	-0.365	-0.084	
AA521346 H.sapiens mRNA for Ndr protein kinase AA176957 H.sapiens mRNA for nebulin	-0.169	0.211	0.279	0.298	0.632	0.273	
AA676598 H.sapiens mRNA for nerve growth factor-inducible PC4 homologue	-0.154	0.055	0.231	0.150	0.263	-0.252	
R23251 H.sapiens mRNA for Not56-like protein	0.426 0.255	0.100 0.053	0.091 0.610	0.009 0.427	0.340 0.146	-0.047 1.196	
R27550 H.sapiens mRNA for novel gene in Xq28 region R40059 H.sapiens mRNA for nuclear pore complex protein hnup153	-0.055	-0.071	0.372	0.002	-0.076	0.590	
AA504266 H.sapiens mRNA for nuclear protein SA-2	1.768	0.127	1.645	1.022	0.761	0.344	
W86182 H.sapiens mRNA for nuclear protein SDK3, partial	0.082 0.945	-0.133 0.697	0.735 0.820	0.300 0.454	0.195 0.545	0.455 0.593	
AA485958 H.sapiens mRNA for nucleoporin-like protein	0.945	0.087	-0.309	0.154	0.058	0.396	
H54417 H.sapiens mRNA for nucleoside-diphosphate kinase AA488609 H.sapiens mRNA for Nup88 protein	0.195	0.224	0.343	0.336	0.298	0.273	
AA447727 H.sapiens mRNA for orphan nuclear hormone receptor	-0.282	-0.423	0.218	0.116	0.331 -0.069	0.167 0.305	
AA418466 H.sapiens mRNA for p0071 protein	-0.505 0.308	-0.137 0.183	0.151 0.202	-0.085 0.061	0.094	-0.071	
AA778919 H.sapiens mRNA for P2Y6 receptor AA481759 H.sapiens mRNA for p35, cyclin-like CAK1-associated protein	-0.416	0.085	0.039	-0.302	0.822	0.696	
R59621 H.sapiens mRNA for p40	-0.190	-0.081	0.151	-0.208	-0.391	0.053 -0.225	
AA465389 H.sapiens mRNA for p40phox	0.506 0.212	0.128 1.296	0.202 0.167	0.712 -0.499	0.210 1.172	0.029	
AA169832 H.sapiens mRNA for PAPS synthetase H65660 H.sapiens mRNA for peroxisomal acyl-CoA oxidase	-0.159	0.196	0.207	0.309	0.094	-0.824	
H:sapiens mRNA for peroxisomal acyr-CoA oxidase AA489201 H:sapiens mRNA for PHAPI2b protein	-0.111	0.170	0.135	0.511	-0.047	0.016	
N67038 H.sapiens mRNA for phenylalkylamine binding protein	0.604	0.287	1.887 0.136	1.023 0.181	2.513 0.167	0.196 0.254	
AA146803 H.sapiens mRNA for phosphate cyclase	-0.248	0.267	Ų. 130	Ų. 10 I	0.107	Q.204	

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ACC Gene Name AA456101 H.sapiens mRNA for phosphatidylinositol 3-kinase	ZR75 0.028	YY3 0.129	-0.040	468 0.014	MPI 0.515	231 0.577	(log base 2 ratio
AA186901 H.sapiens mRNA for phosphoenolpyruvate carboxykinase	0.519	0.156	0.836	-0.346 0.381	0.131 0.536	0.681	
AA699876 H.sapiens mRNA for phosphoinositide 3-kinase AA476263 H.sapiens mRNA for phosphorylase-kinase, beta subunit	0.097 -0.014	0.707 -0.317	0.443 0.134	-0.398	0.267	0.163	
H69335 H.sapiens mRNA for Pirin, isolate 1	1.500	0.886	0.281	1.184	0.613 0.302	-0.066 -0.055	
H66158 H.sapiens mRNA for plakophilin 2a and b	-0.345 -1.331	0.104 -0.729	-0.077 -0.184	-0.223 -0.438	-0.194	-0.483	
AA676223 H.sapiens mRNA for pristancyl-CoA oxidase AA291490 H.sapiens mRNA for processing a-glucosidase I	-0.279	-0.022	0.156	0.024	-0.039	-0.189	
AA115877 H.sapiens mRNA for protease inhibitor 12 (PI12; neuroserpin)	-0.399 -0.565	0.084	0.069 -0.190	0.040 -0.599	0.052 -0.266	0.226 -0.187	
AA452149 H.sapiens mRNA for protein kinase, Dyrk2 AA450003 H.sapiens mRNA for protein kinase, Dyrk4, partial	1.387	0.946	1.519	0.775	1.635	-0.188	
AA521083 H.sapiens mRNA for protein phosphatase 6	-0.070 0.089	0.265 0.099	0.199 0.011	-0.199 0.138	-0.070 0.232	0.698	
R42433 H.sapiens mRNA for protein tyrosine phosphatase H23202 H.sapiens mRNA for protein-tyrosine-phosphatase	0.178	0.254	0.136	-0.151	0.148	-0.078	
AA630374 H.sapiens mRNA for protein-tyrosine-phosphatase (tissue type: foreskin)	-0.253	-0.469	-0.782 -0.376	-0.925 -0.475	-0.145 -0.222	-0.281 0.091	
N52350 H.sapiens mRNA for protein-tyrosine-phosphatase (tissue type: testis) H03504 H.sapiens mRNA for protein-tyrosine-phosphatase D1	0.281 -0.209	0.323 0.117	-0.376	-0.369	-0.110	-0.090	
AA447793 H.sapiens mRNA for pur alpha extended 3'untranslated region	0.407	0.339	0.373	0.042	0.322	0.755 0.627	
H08188 H.sapiens mRNA for putative chloride channel	0.314 0.028	0.315 0.075	0.229	0.301 -0.175	0.260 -0.139	0.027	
R42600 H.sapiens mRNA for putative MT4-MMP protein AA025059 H.sapiens mRNA for Rab11 gene	-0.689	-0.025	-0.336	-0.635	0.068	-0.082	
AA406613 H.sapiens mRNA for ragA protein	0.361 0.121	0.057 0.079	-0.305 0.437	0.340 0.179	0.208 0.536	0.159 0.336	
N73499 H.sapiens mRNA for ragB protein AA485734 H.sapiens mRNA for RanGTPase activating protein 1	0.159	0.245	0.118	0.002	0.359	0.485	
AA482117 H.sapiens mRNA for ras-related GTP-binding protein	0.134 0.273	0.307 1.222	0.345 0.068	0.106 0.336	0.664 -0.455	0.993	
AA476438 H.sapiens mRNA for rat HREV107-like protein AA486281 H.sapiens mRNA for rat translocon-associated protein delta homolog	0.564	0.449	0.284	0.200	0.333	0.369	
AA243749 H.sapiens mRNA for receptor protein tyrosine kinase	2.276	0.247	1.969	0.922 0.345	1.035 0.542	0.532 0.943	
AA459400 H.sapiens mRNA for rho GDP-dissociation Inhibitor 1 AA680244 H.sapiens mRNA for ribosomal protein L11	0.144 -0.358	0.268 -0.197	0.336 0.176	-0.294	-0.073	0.649	
AA027840 H.sapiens mRNA for RIT protein	-0.451	-0.210	-0.281	-0.608	-0.181	-0.025 0.447	
R08935 H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)	0.404 -0.257	1.095 -0.290	0.497 -0.351	0.683 0.294	0.561 -0:334	0.334	
AA019549 H.sapiens mRNA for RP3 gene N66132 H.sapiens mRNA for rTS beta protein	0.368	0.121	0.884	0.310	1.497	-0.204	
AA070489 H.sapiens mRNA for S100 calcium-binding protein A13	-0.189 0.399	-0.140 0.587	0.136 0.022	0.714 0.379	-0.133 0.108	0.369 0.414	
AA634360 H.sapiens mRNA for Sec23B isoform, 2450bp AA070226 H.sapiens mRNA for selenoprotein P	0.529	0.342	0.365	-0.009	0.293	0.441	
AA488447 H.sapiens mRNA for serine palmitoyltransferase, subunit I	-0.238 -0.284	0.268 -0.159	0.419 0.692	1.035 0.852	0.172 0.011	0.122 0.284	
W61116 H.sapiens mRNA for serine/threonine protein kinase, NIK H15445 H.sapiens mRNA for SEX gene	0.684	0.720	0.182	0.928	-0.308	0.221	
R33031 H.sapiens mRNA for sigma 3B protein	-0.213	0.066	0.337 0.342	-0.097 0.394	-0.118 0.606	0.273 0.048	
AA481555 H.sapiens mRNA for skeletal muscle abundant protein AA426053 H.sapiens mRNA for skeletal muscle-specific calpain	0.701 -0.197	0.413 -0.129	-0.052	-0.385	-0.184	0.251	
AA668189 H.sapiens mRNA for Sm protein F	0.446	0.366	-0.044	0.412 0.414	0.127 0.066	0.519 1.005	
AA133577 H.sapiens mRNA for Sm protein G	0.320 -0.292	0.784 -0.572	0.006 -0.669	0.046	0.241	0.587	
AA872379 H.sapiens mRNA for SMT3A protein AA775415 H.sapiens mRNA for SMT3B protein	0.114	0.298	0.459	0.989	0.086	0.566 0.310	
AA490209 H.sapiens mRNA for Sop2p-like protein	0.039 1.042	0.379	0.279 0.274	0.262 0.334	0.454 0.276	0.310	
AA136125 H.sapiens mRNA for spermine synthase R38682 H.sapiens mRNA for splicing factor SF3a120	0.371	1.092	0.762	0.093	-0.068	0.873	
T72628 H.sapiens mRNA for splicing factor SF3a120	0.355 0.315	-0.132 0.806	0.490 0.012	-0.103 0.311	0.520 -0.049	0.446 0.283	
R38682 H.sapiens mRNA for splicing factor SF3a120 R39069 H.sapiens mRNA for STM-7 protein	0.766	-0.234	0.227	0.358	-0.546	0.103	
AA156461 H sapiens mRNA for surface glycoprotein	-0.199 0.169	-0.189 -0.006	0.247 0.079	-0.198 -0.638	-0.250 -0.244	0.035 0.358	
N59206 H.sapiens mRNA for SYT AA279440 H.sapiens mRNA for tafazzins protein	0.103	0.708	0.232	0.044	0.277	0.638	
R97095 H.sapiens mRNA for Tcell leukemia/lymphoma 1	0.333 -0.178	0.583 0.104	0.100 0.254	0.294 -0.132	-0.082 0.003	0.312	
AA699317 H.sapiens mRNA for testican R60847 H.sapiens mRNA for TFG protein	0.474	0.633	-0.018	0.192	-0.309	0.538	
R83270 H.sapiens mRNA for TGIF protein	-0.308	-0.133 0.461	0.104 0.435	0.023 -0.149	-0.381 0.572	0.796 0.587	
H68845 H.sapiens mRNA for thiol-specific antioxidant AA708446 H.sapiens mRNA for TIM17 preprotein translocase	0.538 -0.184	0.127	0.446	0.363	0.059	0.464	
H15707 H.sapiens mRNA for TRAMP protein	-0.158	-0.197	0.019 0.334	0.076 -0.060	-0.195 0.485	0.323 0.184	
AA487434 H.sapiens mRNA for transcript associated with monocyte to macrophage differentiation N92711 H.sapiens mRNA for transcription factor TFIID subunit TAFII28	0.820 0.166	0.644 -0.077	0.065	0.134	0.209	0.222	
N92711 H.sapiens mRNA for transcription factor THID subunit TAPII26 AA460927 H.sapiens mRNA for translin	0.453	0.474	-0.340	-0.484	0.096	0.362 0.410	
AA477514 H.sapiens mRNA for translin associated protein X	-0.050 0.051	-0.592 0.218	-0.208 0.685	-0.891 0.657	-0.338 0.119	0.779	
AA476282 H.sapiens mRNA for transmembrane protein mp24 AA709143 H.sapiens mRNA for TTF-I	0.084	0.303	0.099	0.238	0.818	0.304	
AA130874 H. sapiens mRNA for tyrosine phosphatase	0.442 -0.431	0.214 -0.271	0.064 -0.145	0.189 -0.447	0.315 0.160	0.647	
AA044025 H.sapiens mRNA for ubiquitin conjugating enzyme, UbcH6 H13688 H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase	0.023	0.677	-0.291	0.143	0.062	0.702	
AA706987 H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)	0.129 -0.022	0.215 -0.019	0.375	0.087 0.263	0.008 0.167	-0.132	
AA099568 H.sapiens mRNA for uridine phosphorylase AA489017 H.sapiens mRNA for USF2a & USF2b, clone P9DH	-0.109	-0.068	-0.168	-0.445	-0.362	0.458	
AA397823 H.sapiens mRNA for ZID protein	0.434 -0.360	0.555 -0.505	0.138 -0.080	0.281 -0.437	-0.265 -1.101	.0.315 0.060	
W31899 H.sapiens mRNA for zinc finger gene AA489714 H.sapiens mRNA for ZYG homologue	-0.515	-0.220	-0.473	-0.565	-0.792	0.058	
AA464198 H.sapiens mRNA PSSALRE for serine/threonine protein kinase	0.704 0.122	0.347 0.091	0.513 0.084	0.371 0.286	0.471 0.195	0.382 0.479	
AA490501 H.sapiens mRNA; UV Radiation Resistance Associated Gene AA421518 H.sapiens mRNS for clathrin-associated protein	-0.180	-0.332	-0.275	-0.097	-0.073	0.546	
AA029308 H.sapiens MTCP1 gene, exons 2A to 7 (and joined mRNA)	0.175 0.552	-0.281 0.315	-0.412 0.332	-0.449 0.423	-0.118 0.125	0.565 0.418	
AA448256 H.sapiens MTF-1 mRNA for metal-regulatory transcription factor AA167113 H.sapiens NAP (nucleosome assembly protein) mRNA, complete cds	-0.033	-0.133	0.825	0.330	0.202	0.289	
W93379 H.sapiens nek2 mRNA for protein kinase	-0.862	0.017	-0.324	-0.813 -0.188	-0.453 0.259	0.732 0.184	
AA425336 H.sapiens NF-H gene, exon 1 (and joined CDS) AA598659 H.sapiens NuMA gene (Clone T33)	-0.171 -0.175	0.103 0.427	0.136 0.035	-0.963	-0.390	-0.049	
H51066 H.sapiens OB-RGRP gene	0.873	0.602	-0.130	-0.472	-0.219 -0.110	0.305 0.127	
T67066 H.sapiens OXA1Hs mRNA	0.254 -0.002	0.361 0.279	-0.037 0.568	0.014 0.447	0.373	-0.081	
AA504351 H.sapiens OZF mRNA AA598787 H.sapiens p63 mRNA for transmembrane protein	0.345	0.218	0.198	-0.311	0.273	0.665	
AA100296 H.sapiens PAP mRNA	0.387 0.071	-0.249 0.739	-0.397 1.116	-0.249 0.022	-0.205 0.924	0.619 0.812	
H70484 H.sapiens partial C1 mRNA AA405767 H.sapiens Pax8 mRNA	0.511	0.825	0.121	-0.047	0.698	0.958	
N67778 H.sapiens PEBP2aC1 acute myeloid leukaemia mRNA	-0.533 0.433	0.507 1.119	-0.015 -0.191	-0.662 0.360	-0.161 -0.100	0.531 0.046	
AA911971 H.sapiens PRR1 mRNA H48425 H.sapiens Pur (pur-alpha) mRNA, complete cds	0.411	0.031	-0.008	-0.263	-0.451	0.602	
W05696 H.sapiens ray mRNA	0.049 -0.282	0.126 -0.086	0.164 -0.372	-0.270 -0.010	-0.263 -0.082	0.289 -0.420	
AA016290 H.sapiens RBQ-1 mRNA AA057436 H.sapiens RFXAP mRNA	0.254	0.443	0.428	1.043	0.268	0.137	
AA293192 H.sapiens RY-1 mRNA for putative nucleic acid binding protein	0.881 -0.429	0.680 1.495	0.235 0.152	0.738 0.073	1.148 1.724	-0.057 0.418	
AA458884 H.sapiens S100A2 gene, exon 1, 2 and 3 N73827 H.sapiens SA mRNA	-0.978	-0.505	-0.665	-0.594	-0.178	0.364	
AA459351 H.sapiens sds22-like mRNA	0.498 0.541	0.470 0.697	0.810 0.464	0.164 0.184	1.054 0.187	0.649 0.507	
AA459363 H.sapiens seb4D mRNA H51554 H.sapiens Ski-W mRNA for helicase	-0.602	-0.475	-0.595	-0.706	-0.498	-0.288	

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		ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
ACC H93121	Gene Name H.sapiens Sp17 gene	-0.253	0.213	0.516	0.156	0.173	0.958	(log base 1 lane
R51052	H.sapiens SPHAR gene for cyclin-related protein	-0.093	0.281	-0.019	0.048	-0.496	0.221	
	H.sapiens Staf50 mRNA	-0.327 0.218	-0.058 0.252	0.593 0.212	0.415 -0.164	0.188 -0.032	0.385 -0.997	
AA459247 H39018	H.sapiens SURF-5 mRNA H.sapiens Syt V gene (genomic and cDNA sequence)	0.341	0.161	0.155	0.346	0.139	0.120	
AA403035	H.sapiens TFE3 gene, exons 1,2,3 (and joined CDS)	0.347	0.006	0.118	0.167	0.377	-0.043	
N90273	H.sapiens TTF mRNA for small G protein	-0.473 -0.182	-0.976 -0.192	-0.049 0.490	-0.147 0.408	-0.974 -0.310	0.421 0.345	
	H.sapiens YPT3 mRNA H.sapiens ZNF183 gene	-0.089	0.253	-0.246	-0.344	-0.001	0.614	
AA448396	Heat shock 10 kD protein 1 (chaperonin 10)	0.434	0.201	0.271	0.516	0.744	1.070	
R01139	Heat shock 27kD protein 1	0.521 0.180	0.492 0.044	-0.167 -0.111	-0.294 -0.236	0.894 0.169	0.065 -0.354	
	Heat shock 60 kD protein 1 (chaperonin) HEAT SHOCK 70 KD PROTEIN 1	-0.219	-0.120	0.082	0.138	0.003	0.029	
AA629567	HEAT SHOCK COGNATE 71 KD PROTEIN	-0.143	0.303	0.564	-0.302	0.174	0.199	
AA449119	HEAT SHOCK FACTOR PROTEIN 1	0.141	0.172	0.349 0.121	-0.050 -0.002	-0.072 0.307	0.774 -0.047	
AA253434	HEAT SHOCK FACTOR PROTEIN 2 HEAT SHOCK PROTEIN HSP 90-ALPHA	0.015 -0.278	0.062 0.038	0.302	-0.254	-0.359	0.219	
W51795	Heat shock protein HSP72 homolog [human, thyroid associated ophthalmopathy patient, mRNA Partial	0.231	-0.138	0.475	-0.043	0.494	0.456	
AA278759	Hematopoetic proteoglycan core protein	1.420	0.997	0.341	-0.028	1.098 0.830	0.911 0.608	
	HEMATOPOIETIC LINEAGE CELL SPECIFIC PROTEIN	-0.274 0.227	1.014 0.367	0.027 0.165	0.626	0.350	0.836	
T71606	Heme oxygenase (decycling) 1 Heme oxygenase (decycling) 2	-0.277	-0.064	-0.366	-0.157	-0.306	0.938	
	HEMOGLOBIN EPSILON CHAIN	0.161	0.683	-0.207	-0.093	0.401	0.718 1.291	
N95121	Hemoglobin gamma-G	-0.311 -0.447	0.938 -0.374	-0.661 0.074	-0.857 -0.234	-0.736 -0.097	0.551	
	HEMOGLOBÍN ZETA CHAIN	0.100	0.953	0.097	-0.071	0.164	1.282	
AA149097	Hemoglobin, alpha 1 Hemopoietic cell kinase	0.468	0.278	0.319	0.445	0.934	0.613	
AA463635	Heparan sulfate-N-deacetylase/N-sulfotransferase	0.749 0.566	0.596 0.396	0.133 0.184	0.207 0.297	0.442 0.502	0.146 0.415	
	Heparin cofactor II	0.475	0.612	0.169	0.091	0.484	0.311	
N70235 R52798	Hepatic leukemia factor Hepatocyte growth factor (hepapoletin A; scatter factor)	0.409	0.743	0.433	0.333	0.893	0.001	
H62163	Hepsin	0.860	0.406	0.618	0.445	0.400	-0.529 0.485	
AA418683	Hermansky-Pudlak syndrome protein	0.543 0.410	0.605 0.346	0.005 0.296	0.169 0.189	0.394 0.694	0.885	
AA192411	HETEROCHROMATIN PROTEIN 1 HOMOLOG Heterogeneous nuclear ribonucleoprotein A1	0.471	0.390	0.040	0.010	0.852	1.077	
W02101	Heterogeneous nuclear ribonucleoprotein A2/B1	0.367	0.482	0.039	0.267	0.300	0.651	
AA487442	Heterogeneous nuclear ribonucleoprotein G	0.728	0.501 0.391	0.539 0.335	0.384 0.518	0.915 0.010	-0.347 0.535	
W85697	Heterogeneous nuclear ribonucleoprotein K HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN L	0.067 -0.054	0.052	0.074	0.389	-0.294	0.763	
AA498792	HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U	0.364	0.736	0.363	0.431	0.108	0.994	
R39239	Hexabrachion (tenascin C, cytotactin)	0.715	0.700	0.158	0.330	0.454 -0.446	0.730 0.574	
AA485272	Hexokinase 1	-0.458 0.006	-0.455 0.357	-0.173 -0.677	-0.107 -0.720	-0.446	-0.316	
T63321	Hexosaminidase B (beta polypeptide) High mobility group (nonhistone chromosomal) protein isoforms I and Y	0.506	0.201	0.071	0.330	0.613	-0.036	
R14855	High mobility group box	0.574	0.352	0.229	0.323	0.258	0.661	
AA683085	High-mobility group (nonhistone chromosomal) protein 1	0.140 0.922	0.198 1.020	-0.193 0.337	0.135 0.386	0.277 0.305	0.904	
	High-mobility group (nonhistone chromosomal) protein 2	0.865	1.115	0.290	0.110	0.697	0.539	
H18971 W86776	Hippocalcin Histidine ammonia-lyase	-0.045	0.053	-0.487	-0.198	0.014	-0.080	
H70473	Histidine-rich glycoprotein	0.596	0.615	0.577 0.277	0.084 0.392	0.400 1.224	0.754 0.488	
H61209	Histidyl-tRNA synthetase	1.125 0.074	0.641 0.611	0.181	-0.084	0.977	0.356	
T66815 H95392	HISTONE H2A.X	0.586	0.149	0.572	0.180	0.065	0.106	
	HISTONE H3.3	-0.032	0.067	0.412	-0.047	-0.002	0.782	
AA668811	HISTONE H3.3	-0.202 0.297	0.376 0.614	-0.248 0.357	0.424 0.319	0.121 0.068	0.928 0.686	
R37224	HKR-T1 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN PRECURSOR	0.129	-0.084	0.078	0.299	0.186	0.790	
R47979	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR ALPHA CHAIN PRECURSOR	0.623	0.086	0.442	0.054	0.157	1.011	
AA455043	Holocarboxylase synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	0.446 0.686	0.395 0.753	0.423 0.022	0.125 -0.070	0.278 0.725	0.872 0.034	
	Homeo box A4	1.170	1.061	0.530	0.559	1.090	0.616	
H02243	Homeo box A9 Homeo box B5 (2.1 protein)	1.324	0.990	0.075	0.953	1.036	0.702	
AA706301	HOMEOBOX PROTEIN HOX-A5	0.711	0.897 0.420	1.014 0.111	1.182 0.429	0.850 0.229	0.833 0.351	
AA610066	HOMEOBOX PROTEIN HOX-B6	0.447 0.465	0.420	0.491	0.089	0.079	0.214	
AA411169 AA428196	HOMEOBOX PROTEIN HOX-D3 HOMEOBOX/POU DOMAIN PROTEIN RDC-1	0.008	0.011	0.275	0.694	0.391	0.620	
R62603	Homo sapien, alpha-3 (VI) collagen	0.795	0.551	0.727	0.622	0.550	0.918 1.028	
R37768	Homo sapiens (clone 13a) deoxyhypusine synthase mRNA, complete cds	-0.221 0.258	-0.051 -0.002	-0.208 -0.266	0.009 -0.323	0.224 -0.201	0.608	
R37766	Homo sapiens (clone 13a) deoxyhypusine synthase mRNA, complete cds Homo sapiens (clone CC6) NADH-ubiquinone oxidoreductase subunit mRNA, 3' end cds	-0.804	-0.155	-0.628	-0.967	-0.575	0.673	
AA426374	Homo sapiens (clone ch13lambda7) alpha-tubulin mRNA, complete cds	0.157	-0.053	0.393	0.121	0.347	0.580	•
AA757351	Homo sapiens (clone HSNME29) CGRP type 1 receptor mRNA, complete cds	-0.145	0.088	0.270 0.031	0.445 -0.768	0.228 -0.327	-0.173 -0.053	
AA460830	Homo sapiens (clone mf.18) RNA polymerase II mRNA, complete cds Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3'	0.052 0.753	0.039 0.456	0.352	0.349	0.695	0.747	
AA789328	Homo Sapiens (clone PK2J) CDC2-related protein kinase (PISSLRE) mRNA, complete cds	-1.524	-0.654	-1.043	-0.703	-1.394	0.684	
A A 479490	Homo seniens (np21) mRNA complete cds	-0.547	-0.504	-0.409 0.108	-0.955 -0.278	-0.741 0.323	0.455 0.163	
AA877669	Homo sapiens 130 kD Golgi-localized phosphoprotein (GPP130) mRNA, complete cds	0.027 0.539	0.126 0.367	0.115	0.310	0.429	0.392	
AA262074 AAAA4568	Homo sapiens 1C7 precursor, mRNA, alternatively spliced, complete cds Homo sapiens 26S proteasome ATPase subunit mRNA, complete cds	0.209	0.276	-0.069	-0.488	-0.107	0.838	
N22904	Homo saniens 3-phosphoinositide dependent protein kinase-1 (PDK1) mKNA, complete cos	0.251	-0.342	0.044	-0.005	0.354	0.764	
N66028	Homo sapiens 48 kDa FKBP-associated protein FAP48 mRNA, complete cds	0.271 0.531	0.348 0.168	0.461 -0.008	0.521 0.205	0.173 0.540	0.824 0.743	
AA777551 R00855	Homo sapiens 5,10-methenyttetrahydrofolate synthetase mRNA, complete cds Homo sapiens 59 protein mRNA, 3' end	0.742	1.078	-0.680	0.003	0.738	0.988	
H54020	Homo sapiens 9G8 splicing factor mRNA, complete cds	-0.259	-0.077	-0.242	-0.046	0.076	0.856	
R40057	Homo saniens AC133 antigen mRNA, complete cds	0.385 -0.220	-0.069 -0.209	0.265 1.023	-0.372 1.640	0.395 -0.337	0.801 0.831	
AA032090	Homo sapiens actin-related protein Arp2 (ARP2) mRNA, complete cds Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds	0.012	0.056	-0.001	-0.140	-0.266	0.699	
W69399	Homo sapiens adenosine triphosphatase mRNA, complete cds	0.164	0.283	0.416	0.742	0.399	1.142	
R37953	Homo sapiens adenylyt cyclase-associated protein (CAP) mRNA, complete cds	0.269	0.272	-0.118	-0.487	-0.001	0.952 0.950	
R37953	Homo sapiens adenylyl cyclase-associated protein (CAP) mRNA, complete cds	-0.081 0.247	0.101 1.771	0.021 1.309	-0.169 1.106	-0.051 1.573	-0.780	
AA460823 T62865	Homo sapiens adhalin-35 mRNA, complete cds Homo sapiens aflatoxin aldehyde reductase AFAR mRNA, complete cds	0.016	0.135	0.154	0.405	-0.249	-0.209	
AA458878	Homo sapiens agrin precursor mRNA, partial cds	0.465	0.456	0.075	0.322	0.192	0.810	
R89082	Homo sapiens A-kinase anchoring protein (AKAP18) mRNA, complete cds	0.057 -0.061	0.614 -0.173	0.145 -0.008	-0.208 -0.543	0.272 -0.293	0.866 1.050	
N53512	Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds Homo sapiens alpha SNAP mRNA, complete cds	0.371	0.531	0.134	0.059	0.417	0.915	
H45455	Homo sapiens alpha-mannosidase (6A8) mRNA, complete cds	-0.198	-0.004	-0.086	0.318	-0.231	1.019	
H15703	Homo sapiens ALR mRNA, complete cds	-0.030 0.305	-0.124 0.845	0.378 0.452	0.238 -0.125	0.060 1.069	0.577 0.870	
AA453175	Homo sapiens amphiphysin II mRNA, complete cds Homo sapiens Amplified in Breast Cancer (AIB1) mRNA, complete cds	0.305 0.167	0.845	0.452	-0.125	0.115	0.825	
AA456636	Homo sapiens androgen receptor associated protein 24 (ARA24) mRNA, complete cds	0.571	0.327	0.334	0.083	0.192	0.734	
AA452848	Homo sapiens angio-associated migratory cell protein (AAMP) mRNA, complete cos	-0.215	0.156	-0.292 -0.939	-0.863 -1.157	-0.116 -0.819	0.224	•
AA125872	Homo sapiens angiopoletin-2 mRNA, complete cds Homo sapiens apoptosis-related protein TFAR15 (TFAR15) mRNA, complete cds	-0.445 -0.157	-0.328 -0.206	0.472	0.397	0.269	-0.009	
R68555 N51014	Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds	0.275	0.814	0.090	0.168	0.372	0.489	
AA621132	Homo sapiens AQP9 mRNA for aquaporin 9, complete cds	0.262	0.425	0.197	-0.106	0.200	0.882	

ACC	Gene Name	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
AA142922	Homo sapiens Arg/Abl-interacting protein ArgBP2a (ArgBP2a) mRNA, complete cds	0.002	0.318	-0.133	0.308	0.171 0.490	0.797 0.832	
W55964	Homo sapiens Aro2/3 protein complex subunit p16-Arc (ARC16) mRNA, complete cds	0.135 0.630	0.388 0.318	0.082 1.037	0.291 0.275	1.040	0.462	
H54627	Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds	-0.100	0.218	0.057	-0.318	0.033	0.525	
H73276 H25917	Homo sapiens Arp2/3 protein complex subunit p21-Arc (ARC21) mRNA, complete cds Homo sapiens Arp2/3 protein complex subunit p34-Arc (ARC34) mRNA, complete cds	1.800	0.858	0.958	0.484	1.176	0.881	
AA188179	Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds	0.182	0.150	0.214	-0.023	0.256	0.698	
AA504809	Homo sapiens arsenite translocating ATPase (ASNA1) mRNA, complete cds	0.230	0.317	0.042	-0.118 0.363	0.057 0.291	0.895 1.942	
AA055486	Horno sapiens ataxia-telangiectasia group D-associated protein mRNA, complete cds	0.810 0.144	0.769 0.464	-0.004 0.007	0.602	-0.006	0.385	
W87752	Homo sapiens ATF family member ATF6 (ATF6) mRNA, complete cds	-0.055	0.134	0.226	0.054	0.145	0.633	
AA448286	Homo sapiens atrophin-1 interacting protein 4 (AIP4) mRNA, partial cds Homo sapiens autoantigen mRNA, complete cds	0.077	-0.117	-0.362	-0.908	-0.205	0.701	
AA447593	Homo sapiens axonemal dynein light chain (hp28) mRNA, complete cds	0.414	-0.024	0.396	0.263	0.082	0.356	
AA410383	Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds	-0.238	0.214	0.252	0.054	-0.231 -0.065	0.641 0.509	
AA599120	Homo sapiens BAF57 (BAF57) gene, complete cds	-0.305 0.169	-0.072 0.552	0.124 -0.139	-0.178 0.518	-0.003	0.534	
H17398	Homo sapiens BAI 3 mRNA, complete cds Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory	-0.173	-0.275	-0.194	0.368	0.137	0.859	
W72437	Homo sapiens BC-2 protein mRNA, complete cds	0.199	0.248	0.203	0.177	0.558	-0.035	
N25578 N62514	Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 2 (BNIP2) mRNA, complete cds	0.307	0.142	0.061	0.146	0.421	0.410	
H54289	Homo sapiens Bet1p homolog (hbet1) mRNA, complete cds	0.286	0.595	-0.006	0.055	0.937 -0.417	-0.643 0.559	
AA429882	Homo sapiens bet3 (BET3) mRNA, complete cds	-0.114 0.340	-0.406 0.717	0.066 -0.162	-0.123 0.326	0.010	0.672	
AA678280	Homo sapiens beta-3A-adaptin subunit of the AP-3 complex mRNA, complete cds	0.164	0.656	-0.283	0.080	-0.178	0.310	
AA159359	Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds Homo sapiens bicaudal-D (BICD) mRNA, complete cds	0.611	0.397	0.402	0.125	0.495	-0.190	
AA035095	Homo sapiens breakpoint cluster region protein 1 (BCRG1) mRNA, complete cds	-0.121	0.185	0.125	0.043	0.553	0.217	
AA443638	Homo sapiens breast cancer-specific protein 1 (BCSG1) mRNA, complete cds	-0.209	-0.684	-0.253	-0.413 0.590	-0.016 -0.280	0.027 0.778	
AA701929	Homo sapiens bystin mRNA, complete cds	0.076 0.305	0.382 0.704	-0.281 0.148	0.496	0.863	0.729	
R22179	Homo sapiens CAGF28 mRNA, partial cds	0.008	0.290	0.405	0.024	0.174	0.968	
N57754	Homo sapiens CAGH1a (CAGH1) mRNA, partial cds Homo sapiens CAGH3 mRNA, complete cds	-0.582	-0.134	-0.879	-0.385	-0.406	0.181	
AA427519	Homo sapiens CAGH32 mRNA, partial cds	-0.112	0.064	0.685	0.207	0.430	0.020	
R53527	Homo sapiens CAGH4 mRNA, partial cds	0.093	0.393	0.218	-0.138 -0.372	0.634 0.098	0.405 0.463	
AA056626	Homo sapiens calcium/calmodulin-dependent protein kinase II mRNA, partial cds	-0.196 0.221	0.010 0.696	0.167 0.085	0.247	0.335	0.231	
AA491238	Homo sapiens calcium-activated potassium channel (SKCA3) mRNA, complete cds	0.243	1.217	0.027	0.417	0.186	0.960	
AA457238 R78585	Homo sapiens calpamodulin (CalpM) mRNA, complete cds Homo sapiens calumenin mRNA, complete cds	0.640	0.989	0.167	0.770	1.208	0.708	
H29322	Homo sapiens cam kinase I mRNA, complete cds	-0.082	0.130	0.130	-0.331	0.246	0.405	
AA463631	Homo sapiens CaM kinase II isoform mRNA, complete cds	0.417	-0.447	-0.597	0.119	-0.276 0.842	0.881 0.763	
T50699	Homo sapiens cancer associated surface antigen (RCAS1) mRNA, complete cds	0.069 -0.256	0.650 -0.638	-0.054 -0.159	-0.212 -1.198	0.098	0.967	
AA171613	Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds	0.123	0.308	-0.029	0.265	0.001	0.907	
AA427725	Homo sapiens carboxypeptidase Z precursor, mRNA, complete cds Homo sapiens casein kinase I gamma 2 mRNA, complete cds	0.440	0.153	-0.387	-0.185	-0.316	0.738	
AA045965	Homo sapiens CASK mRNA, complete cds	0.118	0.285	0.353	1.003	0.266	0.820	
R44202	Homo sapiens catechol-O-methyltransferase (COMT) mRNA, complete cds	-0.189	0.032	0.211	0.035	-0.163	-0.005 -0.013	,
R44202	Homo sapiens catechol-O-methyltransferase (COMT) mRNA, complete cds	0.924	0.691	0.446 0.248	0.156 -0.145	0.336 1.031	0.454	
T89391	Homo sapiens caveolin-2 mRNA, complete cds	0.117 0.114	0.555 0.764	0.038	-0.144	0.347	0.890	
	Homo sapiens CC3 (CC3) mRNA, complete cds Homo sapiens cdc14 homolog mRNA, complete cds	0.336	-0.082	0.141	0.345	-0.021	0.233	
N68854 AA487206	Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT)	-0.113	0.068	-0.007	0.487	0.185	0.967	
AA451903	Homo sapiens cDNA similar to RNA binding protein C. elegans, complete	0.302	0.235	0.048	0.028 0.490	0.113 -0.194	0.792 0.578	
AA676387	Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds	0.045 0.421	0.880 0.899	-0.013 0.133	0.490	0.349	1.337	
	Homo sapiens cell matrix adhesion regulator variant (CMAR) mRNA, complete cds Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds	0.240	-0.208	0.024	-0.075	0.250	0.941	
R87989	Homo sapiens CEV14 mRNA, partial cds	0.507	0.977	0.548	0.813	0.225	0.920	
N65968	Homo sapiens CG1 mRNA, complete cds	-0.093	0.076	0.112	-0.161	-0.048	1.005	
AA417919	Homo sapiens cGMP phosphodiesterase delta subunit mRNA, complete cds	1.702	0.271	1.098	0.097 0.262	0.187 0.145	1.679 0.891	
N38959	Homo sapiens chaperonin containing t-complex polypeptide 1, beta subunit (Cctb) mRNA, complete cd	0.846 0.135	0.818 0.782	0.352 0.155	-0.132	-0.223	0.562	
	Homo sapiens chaperonin containing t-complex polypeptide 1, eta subunit (Ccth) mRNA, complete cds Homo sapiens CHD1 mRNA, complete cds	0.155	0.654	0.342	0.028	0.716	0.572	
H99736 N49703	Homo sapiens CHD1 mRNA, complete cds	0.204	0.711	0.480	-0.032	0.634	-0.208	
AA778077	Homo sapiens CHD3 mRNA, complete cds	0.026	0.142	0.086	-0.089	0.203	0.872 1.364	
N53057	Homo sapiens checkpoint kinase Chk1 (CHK1) mRNA, complete cds	-0.455 0.109	0.165 0.087	0.734 -0.273	0.044 -0.310	0.502 0.227	0.898	
N26062	Homo sapiens chloride channel protein (CiC-2) mRNA, complete cds Homo sapiens chondroitin-6-sulfotransferase mRNA, complete cds	0.149	-0.139	0.084	-0.295	-0.031	0.958	
R15740 T95113	Homo sapiens crondroitin-o-suitotrainsierase mixixa, compete cos Homo sapiens cig5 mRNA, partial sequence	-0.014	0.939	-0.165	0.264	-0.122	1.152	
H11464	Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, con	0.202	0.858	0.044	0.341	-0.185	-0.938	
AA282845	Homo sapiens clk2 mRNA, complete cds	-0.170 0.061	-0.003 0.682	-0.417 0.049	-0.299 0.506	0.003 -0.084	-1.043 -0.165	
AA630459	Homo sapiens clk3 mRNA, complete cds	-0.037	0.307	0.020	0.185	0.199	-0.187	
AA489633	Homo sapiens clone 22 mRNA, alternative splice variant alpha-1, complete cds Homo sapiens clone 23619 phosphoprotein mRNA, partial cds	-0.443	-0.216	-0.689	-1.085	-0.672	0.220	
H23124	Homo sapiens clone 23876 neuronal olfactomedin-related ER localized protein mRNA, partial cds	0.732	-0.501	-0.103	0.111	-0.544	0.466	
AA669222	Homo sapiens clone rasi-1 matrix metalloproteinase RASI-1 mRNA, complete cos	0.207	-0.555	0.455	0.739	1.024	0.341 0.131	
N54848	Homo sapiens coatomer protein (COPA) mRNA, complete cds	-0.434	0.025 0.249	-0.121 0.284	-0.324 0.509	-0.305 0.396	0.131	
R60995	Homo sapiens Coch-5B2 mRNA, complete cds	0.106	0.767	0.378	0.453	0.790	0.733	
N30404	Homo sapiens copper chaperone for superoxide dismutase (CCS) mRNA, complete cds Homo sapiens COX17 mRNA, complete cds	-0.066	-0.050	-0.020	-0.212	-0.322	0.274	
AA186413	Homo sapiens COX4AL mRNA, complete cds	-0.091	0.359	-0.200	0.411	-0.193	-0.183	
AA292226	Homo sapiens creatine transporter mRNA, complete cds	0.260	0.016	0.328	0.119 -0.408	0.453 0.980	0.517 0.151	
	Homo sapiens cyclin G2 mRNA, complete cds	-1.131 0.104	-0.424 0.148	0.704 -0.149	0.084	-0.140	-0.056	
T90767	Homo sapiens cyclin T mRNA, complete cds Homo sapiens cyclin T2a mRNA, complete cds	1.152	0.783	0.216	0.641	0.204	-0.001	
R63702 N78843	Homo sapiens cyclophilin-33A (CYP-33) mRNA, complete cds	-0.033	-0.498	-0.209	-0.392	-0.308	0.606	
AA777187	Homo sapiens Cvr61 mRNA, complete cds	0.518	0.442	0.498	0.651	0.958	0.996	
T59334	Homo sapiens cysteine and glycine-rich protein 2 (CSRP2) mRNA, complete cds	-0.033 0.052	0.167 0.015	-0.412 -0.156	-0.136 0.167	0.232 0.093	0.843 0.558	
W61361	Homo sapiens cytoplasmic antiproteinase 2 (CAP2) mRNA, complete cds	0.032	0.431	0.194	-0.139	-0.142	-0.167	
AA430512 R06254	Homo sapiens cytoplasmic antiproteinase 3 (CAP3) mRNA, complete cds Homo sapiens D54 isoform (hD54) mRNA, partial cds	0.072	0.612	0.324	-0.046	0.468	-0.851	
AA599175	Homo sapiens dbpB-like protein mRNA, complete cds	0.471	0.714	-0.049	0.145	0.584	-0.125	
H84871	Homo sapiens DCHT mRNA, complete cds	0.266	0.103	-0.043 -0.292	-0.127 -0.015	0.292 -0.090	0.126 0.056	
	Homo sapiens dead box, X isoform (DBX) mRNA, alternative transcript 2, complete cds	0.364 0.303	0.302 0.113	0.153	0.056	0.130	-0.133	
AA447588	Homo sapiens dead box, Y isoform (DBY) mRNA, alternative transcript 2, complete cds	0.369	0.612	-0.031	0.084	0.069	0.435	
T71272 H85454	Homo sapiens decoy receptor 1 (DcR1) mRNA, complete cds Homo sapiens delayed-rectifier K+ channel alpha subunit (KCNS1) mRNA, complete cds	1.172	0.897	0.403	0.336	0.727	1.009	
H17139	Homo sapiens delta-catenin mRNA, partial cds	0.302	-0.172	-0.239	-0.060	0.459	0.801	
AA629338	Homo sapiens DGS-A mRNA, 3' end	0.431	0.232	0.390 0.333	0.149 0.575	0.332 0.557	0.670 -1.461	
AA011681	Homo sapiens DGS-D mRNA, 3' end	0.522 0.071	0.381 -0.069	0.333	0.379	0.042	-0.425	
	Homo sapiens DGS-I mRNA, 3' end Homo sapiens di-N-acetylchitobiase mRNA, complete cds	-0.666	-1.270	-1.058	-1.275	-0.661	-0.023	
W33050 AA448866	3 Homo saniens dishevelled 2 (DVL2) mRNA, complete cds	0.245	0.762	0.035	-0.888	-0.380	0.157	
AA705383	Homo sapiens DNA binding protein homolog (DRIL1) mRNA, complete cds	1.007	0.409	0.967	1.286	1.308	-0.021 -0.021	
AA44866	1 Homo saniens DNA polymerase epsilon subunit B (DPE2) mRNA, complete cos	-0.204 0.442	0.116 0.389	-0.087 0.305	0.585 -0.046	0.153 0.324	0.640	
R92124	Home series DNA recombination and repair protein hNgs1 (hNGS1) mKNA, complete cos	0.442	0.006	0.303	-0.046	0.188	0.366	
R64101	Homo sapiens DNA-binding protein (CROC-1A) mRNA, complete cds 3 Homo sapiens DnaJ protein (HSPF2) mRNA, complete cds	0.888	-0.038	0.762	0.705	0.438	0.445	
H12338	Homo sapiens DNAX activation protein 12 (DAP12) mRNA, complete cds	0.759	1.152	0.519	0.721	0.710	0.161	
A 487730	7 Homo sanions DN.13/CPR3 mRNA, complete cds	-0.005	0.234	0.131	-0.001 -0.077	0.143 -0.161	-0.031 -0.465	
AA00475	9 Homo sapiens dolichol monophosphate mannose synthase (DPM1) mRNA, partial cds	0.175	0.394	0.017	-0.077	-0.101	0.700	

ACC	Gene Name Homo sapiens down syndrome candiate region 1 (DSCR1) gene, alternative exon 1, complete cds	ZR75 0.145	-0.463	YY1 -0.404	468 -0.361	MPI -0.111	-0.342	(log base 2 ratio
AA182680	Homo sapiens Drosophila fat facets related Y protein (DFFRY) mRNA, complete cds	0.278	0.224	0.347	-0.047 -0.597	0.094 -0.532	-0.001 0.074	
	Homo sapiens drp1 mRNA, complete cds Homo sapiens dynamin (DNM) mRNA, complete cds	-0.522 0.596	-0.320 0.646	-0.493 0.738	1.636	0.119	-0.159	
AA045529	Homo sapiens dynamin-like protein mRNA, complete cds	0.446	0.405	0.616	0.601	0.488 -0.523	-0.117 0.323	
AA454959	Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds Homo sapiens E1B 19K/Bcl-2-binding protein Nip3 mRNA, nuclear gene encoding mitochondrial protei	-0.479 0.196	-0.692 0.440	-0.372 0.177	-0.839 0.256	0.415	0.323	
W46493	Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds	-0.267	0.494	-0.136	-0.703	0.023	-0.846	
AA001749	Homo sapiens EB1 mRNA, complete cds	0.366 -0.667	0.324 -0.056	0.117 -1.091	-0.084 -0.342	-0.026 -1.033	-0.656 -0.630	
	Homo sapiens EEN-B1 mRNA, complete cds Homo sapiens EEN-B2-L1 mRNA, complete cds	-0.105	0.473	-0.631	0.317	-0.147	-0.581	
AA047039	Homo sapiens efF-1A, Y isoform (EiF1AY) mRNA, complete cds	0.140 0.822	-0.017 0.755	-0.045 0.273	0.060 0.075	0.015 0.835	0.210 -0.291	
R37276	Homo sapiens elF4G1 mRNA, complete cds Homo sapiens elF4Gil mRNA, complete cds	-0.125	-0.057	0.177	-0.334	0.040	-0.068	
H78466	Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds	0.068	0.484	1.103 -0.095	0.613 -0.265	0.711 0.021	0.596 -0.331	
	Homo sapiens endothelial cell protein C/APC receptor (EPCR) mRNA, complete cds Homo sapiens endothelin-1 (EDN1)	0.014 -0.655	0.492 -0.418	-0.418	-0.052	-0.269	0.448	
H11003	Homo sapiens endothelin-1 (EDN1)	0.328	0.516	0.003	0.035	0.096 0.511	-0.355 -0.080	
R48320	Homo sapiens Eph-like receptor tyrosine kinase hEphB1c (EphB1) mRNA, complete cds Homo sapiens epithelial-specific transcription factor ESE-1b (ESE-1) mRNA, complete cds	-0.076 -0.363	0.186 -0.152	0.558 0.126	-0.111 0.099	-0.173	-2.041	
R16667	Homo sapiens eps8 binding protein e3B1 mRNA, complete cds	0.301	0.365	0.711	0.673	0.448	-1.857 -0.133	
AA432066	Homo sapiens epsilon-sarcoglycan mRNA, partial cds Homo sapiens eukaryotic translation initiation factor 3 subunit (p42) mRNA, complete cds	0.408 -0.143	0.806 0.102	-0.062 0.010	0.224 0.333	-0.058	0.418	
AA402440	Homo sapiens exportin t mRNA, complete cds	0.059	0.473	0.174	-0.109	-0.091	-0.312	
AA431813	Homo sapiens EXT like protein 3 (EXTL3) mRNA, complete cds	0.061	0.044 -0.587	0.488	0.224 0.107	0.397 -0.343	0.112 0.042	
AA490078 AA425299	Homo sapiens EXTR2 mRNA, complete cds Homo sapiens ežrin-radixin-moesin binding phosphoprotein-50 mRNA, complete cds	0.221	0.460	-0.036	0.087	0.142	0.416	
AA405989	Homo sapiens Fas-binding protein Daxx mRNA, complete cds	-0.061 0.918	0.030 1.149	0.171 0.264	-0.110 0.587	-0.083 0.566	0.337 -0.217	
AA071526	Homo sapiens fo19 mRNA Homo sapiens FGF-1 intracellular binding protein (FIBP) mRNA, complete cds	0.767	0.912	0.418	1.078	1.083	-1.044	
R08267	Homo sapiens FK-506 binding protein (fkbp12.6) gene, complete cds	-0.291 0.170	-0.579 0.246	-0.976 0.092	-0.882 -0.175	-0.200 0.813	-0.464 -1.959	
AA453766	Homo sapiens FLICE-like inhibitory protein long form mRNA, complete cds Homo sapiens FMRFamide-related prepropeptide mRNA, complete cds	0.544	0.261	0.460	0.052	0.216	-0.839	
AA465236	Homo sapiens forkhead protein (FKHRL1) mRNA, complete cds	0.241	0.249	-0.097	0.159 1.622	0.417 0.990	-0.357 -0.231	
AA113339	Homo sapiens FRG1 mRNA, complete cds Homo sapiens frizzled related protein frpHE mRNA, complete cds	1.791 0.313	1.892 0.724	1.971 -0.024	0.121	0.272	-0.128	
H08753	Homo sapiens G protein beta 5 subunit mRNA, complete cds	0.606	0.803	0.248	0.260	0.273 0.216	-0.127 0.181	
AA419092	Homo sapiens G protein-coupled receptor Edg-4 mRNA, complete cds	0.262 0.373	0.041	0.240 0.287	0.029 0.502	0.109	0.161	
AA010503	Homo sapiens GABA-A receptor delta subunit (GABRD) mRNA, complete cds Homo sapiens gamma SNAP mRNA, complete cds	0.658	0.808	0.119	0.045	0.526	-0.035	
H05619	Homo sapiens GDNF family receptor alpha 2 (GFRalpha2) mRNA, complete cds	0.333 0.403	0.419 0.147	0.211 0.075	0.350 0.722	0.227 0.140	-0.302 -1.667	
R38619 AA488188	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds Homo sapiens gene for protein involved in sexual development, complete cds	0.165	0.228	-0.504	-0.957	0.133	-1.217	
H16573	Homo sapiens germline mRNA sequence	0.609 -0.215	0.950 0.025	0.477 0.162	-0.039 -0.095	0.290 0.227	-1.589 -0.418	
AA152347 R49305	Homo sapiens glutathione transferase (GSTA4) mRNA, complete cds Homo sapiens glycogenin-2 delta (glycogenin-2)	0.077	0.207	0.255	0.166	0.096	-0.760	
R49305	Homo saniens divoggenin-2 delta (divoggenin-2)	0.177 0.042	0.350 0.204	0.184 -0.113	-0.147 0.254	0.226 -0.018	-0.064 -0.462	
H04789	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA, complete cds Homo sapiens GOK (STIM1) mRNA, complete cds	0.165	-0.208	0.316	0.731	-0.062	0.015	
R44140	Homo sapiens Golgi complex autoantigen golgin-97 mRNA, complete cds	1.400 -0.141	-0.075 0.102	1.197 -0.333	1.250 -0.496	0.542 -0.181	0.448 0.437	
	Homo sapiens golgin-245 mRNA, complete cds Homo sapiens Grb14 mRNA, complete cds	-0.565	-0.738	-0.394	-0.655	-0.002	-0.084	
N33574	Homo sapiens growth inhibitor p33ING1 (ING1) mRNA, complete cds	0.217 0.241	0.785 -0.090	0.192 -0.075	0.028 -0.330	0.190 -0.121	0.217 -0.544	
AA461110	Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds Homo sapiens GT197 partial ORF mRNA, 3' end of cds	0.000	0.220	0.199	-0.001	0.564	-0.215	
AA134555	Homo sapiens GT198 mRNA, complete ORF	0.013	-0.300 0.184	-0.234 0.125	0.090 0.174	-0.074 0.769	-0.212 -0.083	
H82977	Homo sapiens GT212 mRNA Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete cds	0.003 0.804	0.171	0.833	0.178	1.358	0.294	
AA775872	Homo saniens GTR2-2 mRNA, complete cds	0.249	0.494	-0.021	0.069 0.522	-0.041 0.179	-0.135 -0.035	
AA431439	Homo sapiens guanylate cyclase activating protein (GCAP) gene, complete cds Homo sapiens hair and skin epidermal-type 12-lipoxygenase-related protein (ALOX12E) mRNA, compl	0.070 0.930	0.430 1.209	0.217 0.215	0.638	0.414	0.228	
AA419264 AA430665	Homo earliege hCPE-R mRNA for CPE-receptor, complete cus	0.472	0.660	0.134	0.418	0.931 -0.564	0.100 0.238	
T55756	Homo sapiens heparan sulfate 3-O-sulfotransferase-1 precursor (3OST1) mRNA, complete cds Homo sapiens hepatocyte nuclear factor 6 (HNF-6) mRNA, partial cds	-0.692 1.399	-0.160 1.267	-0.428 0.097	-0.578 1.225	0.588	0.123	
AA448667	Homo sapiens heterochromatin protein p25 mRNA, complete cds	-0.232	-0.004	0.380	-0.344	0.196	-0.292 -0.325	
AA486402	Homo sapiens heterogeneous nuclear ribonucleoprotein R mRNA, complete cds	-0.220 -0.284	-0.157 -0.505	-0.553 -0.264	-0.991 -0.662	-0.085 -0.466	-0.627	
AA455301 AA625662	Homo sapiens hGAA1 mRNA, complete cds Homo sapiens histone acetyltransferase 1 mRNA, complete cds	0.120	0.638	0.280	0.634	0.255	0.586	
H79779	Homo sapiens histone deacetylase 3 (HDAC3) mRNA, complete cds Homo sapiens histone H2A.2 mRNA, complete cds	0.362 0.421	-0.170 0.743	0.435 0.173	0.305 0.390	0.783 0.615	0.152 0.383	
AA447674	Homo sapiens HIV-Nef associated acyl CoA thioesterase (hNAACTE) mRNA, complete cos	0.510	0.495	-0.020	0.132	0.705	0.007	
R26082	Homo sapiens HKL1 mRNA, complete cds	0.000 -0.105	0.466 0.081	0.342	-0.160 -0.367	0.654 0.203	0.133 0.139	
R08932	Homo sapiens hMed7 (MED7) mRNA, complete cds Homo sapiens HMG box containing protein 1 mRNA, complete cds	0.361	0.459	-0.191	-0.066	0.721	0.071	
R16195	Homo sapiens HNK-1 sulfotransferase mRNA, complete cds	0.000 0.203	0.219 0.163	-0.670 0.208	-0.241 -0.284	-0.670 -0.124	0.047 0.102	
AA490991 AA148641	Homo sapiens HnRNP F protein mRNA, complete cds Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds	0.129	0.905	0.099	-0.315	-0.156	-0.782	
AA479928	Homo sapiens homeodomain protein (OG12) mRNA, complete cds	-0.294 0.213	0.226 0.236	0.097 -0.145	-0.085 0.297	-0.312 0.061	-0.911 -0.567	
AA293653 T54144	Homo sapiens homolog of mouse MAT-1 oncogene mRNA, complete cds Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds	0.082	0.185	0.313	0.837	0.195	-0.385	
AA427954	Homo sapiens hook2 protein (HOOK2) mRNA, complete cds	-0.527 -0.381	-0.308 -0.171	-0.110 0.192	-0.030 0.154	-0.233 -0.214	-0.461 -0.248	
AA679864	Homo sapiens HP protein (HP) mRNA, complete cds Homo sapiens HPV16 E1 protein binding protein mRNA, complete cds	-0.335	-0.262	0.181	-0.250	-0.059	-0.028	
AA434144	Homo sapiens hRVP1 mRNA for RVP1, complete cds	0.351	0.655	-0.385	-0.252 -0.211	-0.480 -1.974	-0.925 -1.753	
AA456621	Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA, complete cds Homo sapiens hyaluronoglucosaminidase 1 (HYAL1) mRNA, complete cds	0.182 0.237	-0.503 0.586	-0.392 0.117	0.318	0.154	-0.787	
R73584	Homo sapiens hydroxysteroid sulfotransferase SULT2B1a (HSST2) mRNA, complete cds	0.630	0.295	0.257	0.387	0.560 0.346	-0.213 -0.457	
H10959	Homo sapiens IB3089A (IB3089A) mRNA, complete cds Homo sapiens importin beta subunit mRNA, complete cds	0.116 -0.121	0.321 -0.099	-0.041 0.423	-0.083 -0.024	-0.059	-0.633	
AA668178	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA, complete cds	0.085	0.320	0.168	0.499	0.169	-0.499	
AA406180	Homo sapiens imprinted multi-membrane spanning polyspecific transporter-related protein (IMPT1) mF Homo sapiens inactive palmitoyl-protein thioesterase-2i (PPT2) mRNA, complete cds	0.183 0.197	0.021 0.208	0.279 0.196	0.116 0.584	0.302 -0.108	-0.868 -0.596	
AA047778	Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c	-0.144	0.177	0.393	0.196	-0.131	-0.589	
H12044	Homo sapiens inducible protein mRNA, complete cds Homo sapiens inner mitochondrial membrane transfocase Tim23 (TIM23) mRNA, nuclear gene encodii	0.116 1.007	0.387 0.242	0.200 0.504	0.282 1.207	0.357 0.471	-0.047 -0.614	
T68317 AA455597	Homo sapiens inositol polyphosphate 4-phosphatase type II-alpha mRNA, complete cos	-0.007	-0.100	0.273	-0.090	-0.265	-1.054	
H59620	Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds	0.340 0.885	0.487 0.797	0.219 0.432	0.263 0.352	0.204 0.353	-0.553 -1.343	
R87964 AA457038	Homo sapiens integrin alpha 8 subunit mRNA, 3' end Homo sapiens integrin cytoplasmic domain associated protein (Icap-1a) mRNA, complete cds	-0.342	1.387	-0.417	-0.469	-0.569	0.076	
AA148200	Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds	0.342 0.569	-0.110 0.059	-0.116 -0.136	0.381 0.230	-0.130 0.186	0.011 -0.497	
68421420	Homo sapiens interferon-inducible protein (AIM2) mRNA, complete cds Homo sapiens interfeukin-1 receptor-associated kinase (IRAK) mRNA, complete cds	0.682	0.281	0.386	0.445	0.424	-0.508	
AA443903	Homo sapiens intermediate conductance calcium-activated potassium channel (nk-ca+) mkNA, comple	-0.058 -0.069	-0.015 0.549	0.011 0.196	-0.588 0.038	0.205 0.431	-0.359 -0.208	
H38839 H20547	Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMPG1) mRNA, complete cds Homo sapiens inwardly rectifying potassium channel (Kir3.2) mRNA, complete cds	0.722	0.623	0.204	0.569	0.598	-0.369	
H68885	Homo sapiens IPL (IPL) mRNA, complete cds	0.116	-0.112	0.389	-0.251	0.226	0.060	

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ACC	Gene Name	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
H93310	Homo sapiens IPW mRNA sequence	0.337 -0.124	0.351 0.215	-0.330 0.179	-0.254 -0.021	0.374 0.045	-0.216 0.186	
R70685 R72432	Homo sapiens Jagged 1 (HJ1) mRNA, complete cds Homo sapiens Jagged 2 mRNA, complete cds	0.687	1.347	0.075	-0.226	0.842	-0.455	
H85962	Homo sapiens JNK kinase 2 (JNKK2) mRNA, complete cds Homo sapiens josephin MJD1 mRNA, complete cds	0.881 0.262	1.349 0.093	0.824 -0.081	0.125 0.164	0.778 -0.020	-0.261 0.064	
AA013095	Homo sapiens K+ channel beta-subunit (Kvb1.3) mRNA, complete cds	0.520	0.543	0.422	0.261	0.710	0.299	
N58558	Homo sapiens kallistatin (Pl4) mRNA, complete cds Homo sapiens karyopherin beta2b homolog mRNA, complete cds	0.491 0.128	0.434 0.186	0.010 0.324	0.832 0.001	0.033 0.648	0.072 0.733	
R08897 AA457696	Homo saniens katanin p80 subunit mRNA, complete cds	0.088	0.475	-0.009	-0.217	-0.124	-0.779	
W93500	Homo sapiens kidney and cardiac voltage dependent K+ channel (KvLQT1) mRNA, complete cds Homo sapiens kinesin-related protein (KIF3C) mRNA, complete cds	-0.416 0.179	0.086 0.255	-0.776 0.076	-0.546 0.727	-0.445 0.172	-0.687 -0.533	
H45668	Homo sapiens Kruppel-like zinc finger protein (EZF) mRNA, complete cds	0.555	0.499	-0.071	0.129	0.288	-0.207 1.142	
	Homo sapiens L-glycerol-3-phosphate:NAD oxidoreductase mRNA, complete cds Homo sapiens LIM homeobox protein cofactor (CLIM) mRNA, complete cds	-1.091 -0.586	-0.865 0.202	-0.443 -1.041	-1.110 -0.232	-1.274 -0.705	0.350	
H73914 N70057	Homo sapiens LST1 mRNA, cLST1/A splice variant, complete cds	0.386	-0.107	0.258	-0.232	0.028 -0.578	-0.075 -0.136	
AA461304	Homo sapiens Luman mRNA, complete cds Homo sapiens lysosomal neuraminidase precursor, mRNA, complete cds	0.201 0.316	-0.107 0.199	-0.113 0.158	-0.653 -0.100	0.117	0.250	
AA664004	Homo sapiens lysosomal pepstatin insensitive protease (CLN2) mkNA, complete cos	0.488	0.412	0.512	1.207	0.549 1.117	0.301 0.048	
AA136707	Homo sapiens lysyl hydroxylase isoform 2 (PLOD2) mRNA, complete cds Homo sapiens m8A methyltransferase (MT-A70) gene, complete cds	0.347 -1.061	0.572 -0.598	1.388 -0.875	0.742 -0.975	-0.348	0.158	
AA485867	Homo sapiens macrophage receptor MARCO mRNA, complete cos	1.490	1.543	0.205 0.039	0.731 -0.329	0.025 -0.192	-0.041 -0.492	
W72201	Homo sapiens mad protein homolog (hMAD-3) mRNA, complete cds Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds	-0.370 0.052	-0.002 0.534	-0.261	0.034	-0.015	-0.426	
R82176	Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds	-0.181	-0.623	-0.930	-1.050	-1.174	-0.072	
	Homo sapiens meltrin-L precursor (ADAM12) mRNA, complete cds Homo sapiens microsomal glutathione S-transferase 2 (MGST2) mRNA, complete cds	-0.214 -0.065	0.142 0.752	-0.082 0.013	-0.135 -0.362	-0.265 0.076	-0.076 0.451	
W73474 AA496565	Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds	0.527	0.228	0.702	1.541	-0.038	0.008 -0.545	
P06626	Homo sapiens MIP-1 delta mRNA, complete cds Homo sapiens mitotic checkpoint kinase Mad3L (MAD3L) mRNA, complete cds	-0.049 0.542	0.459 0.365	-0.300 0.117	-0.049 -0.073	0.313 0.586	0.282	
A A 4 4 6 4 6 2	Homo saniens mitotic checkpoint protein kinase (BUB1) MKNA, complete cos	-0.224	-0.613	-0.753	-0.313	-0.301	0.499	
AA481076	Homo sapiens mitotic feedback control protein Madp2 nomolog mRNA, complete cos	-0.900 1.453	-0.234 0.190	-1.021 1.539	-1.896 0.572	-0.647 1.598	0.752 0.838	
AA705112	Homo sapiens MMS2 (MMS2) mRNA, complete cds Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein A	0.175	0.086	0.364	0.234	0.088	0.586	
AA129777	Homo sapiens monocarboxylate transporter (MCT3) mRNA, complete cos	0.045 0.238	-0.454 -0.007	-0.135 0.034	-0.615 0.515	-0.157 -0.099	0.919 0.428	
H54023	Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds Homo sapiens mRNA capping enzyme (HCE) mRNA, complete cds	0.415	0.652	0.213	0.277	0.361	0.127	
AA410188	Homo sapiens mRNA expressed in osteoblast, complete cds	0.182 1.102	0.793 0.560	0.226 0.127	0.216 0.455	0.242 0.544	0.207 0.036	
AA497055 W74254	Homo sapiens mRNA for 26S proteasome subunit p55, complete cds Homo sapiens mRNA for 36 kDa phosphothyrosine protein	1.629	0.543	2.632	1.049	2.835	0.667	
AA598578	Homo sapiens mRNA for A+U-rich element RNA binding factor, complete cds	-0.304 -0.002	0.048 0.166	-0.155 0.336	0.635 0.154	-0.015 0.523	-0.179 0.266	
AA490462 H51645	Homo sapiens mRNA for AEBP1, complete cds Homo sapiens mRNA for alpha actinin 4, complete cds	-0.070	0.368	-0.502	0.057	0.217	0.510	
AA432271	Homo sapiens mRNA for AMP-activated protein kinase beta 1	-0.399 0.416	-0.082 0.552	0.151 0.014	0.315 0.240	-0.128 0.138	-0.063 0.437	
N78582	Homo sapiens mRNA for AMP-activated protein kinase beta 2 subunit Homo sapiens mRNA for AMY-1, complete cds	-0.247	0.044	0.072	0.291	-0.435	0.661	
R67376	Homo sapiens mRNA for ARNO3 protein	0.441 0.252	0.383 0.250	0.156 0.195	-0.106 -0.098	0.521 0.099	0.195 0.279	
AA085749	Homo sapiens mRNA for ATP binding protein, complete cds Homo sapiens mRNA for ATP synthase subunit e, complete cds	0.317	-0.414	-0.365	0.033	-0.630	0.281	
N74897	Homo sapiens mRNA for ATP-dependent RNA helicase #46, complete cds	0.070 0.467	0.953 0.075	-0.086 -0.127	-0.425 0.322	-0.025 0.220	0.231 -0.428	
R19158	Homo sapiens mRNA for aurora/IPL1-related kinase, complete cds Homo sapiens mRNA for CAB1, complete cds	0.014	0.015	0.218	0.284	0.186	0.465	
AA421819	Homo sapiens mRNA for cadherin-6, complete cds	0.198 -0.003	0.130 0.258	0.699 0.178	-0.208 -0.061	0.047 0.026	0.174 0.611	
AA778675	Homo sapiens mRNA for calmegin, complete cds Homo sapiens mRNA for cardiac calsequestrin, complete cds	-0.067	-0.686	-0.414	0.154	-0.653	0.507	
AA495985	Homo sapiens mRNA for CC chemokine, complete cds	0.419	0.494	0.770 0.173	-0.135 0.163	0.799 0.135	0.216 0.605	
AA443118 R49671	Homo sapiens mRNA for CD151, complete cds Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)	0.167 -0.078	0.061 -0.107	0.235	0.939	-0.021	0.066	
N62245	Homo sapiens mRNA for Cdc7-related kinase, complete cds	-0.374 -0.188	0.057 -0.156	0.364 -0.445	-0.678 -0.615	1.163 -0.237	-0.283 0.175	
AA486435 T58775	Homo sapiens mRNA for CDEP, complete cds Homo sapiens mRNA for chemokine LEC precursor, complete cds	-0.325	0.364	0.042	-0.214	-0.153	0.332	
AA894694	Homo sapiens mRNA for CIRP, complete cds	0.835 -0.106	0.212 -0.099	0.354 0.150	0.625 0.570	0.152 -0.204	0.383 0.492	
R10896 T59055	Homo sapiens mRNA for COX7RP, complete cds Homo sapiens mRNA for CRM1 protein, complete cds	0.052	0.261	0.276	0.121	0.408	0.334	
W94331	Homo sapiens mRNA for cystinosin	-0.487 0.037	-0.271 0.142	-0.255 0.228	-1.193 -0.216	-0.364 0.075	0.826 0.744	
AA062805 W04674	Homo sapiens mRNA for cytochrome b large subunit of complex II, complete cds Homo sapiens mRNA for cytochrome b5, partial cds	0.109	0.145	0.373	-0.197	0.501	0.353	
R97540	Homo sapiens mRNA for DCRA, complete cds	0.035 -0.009	0.010 0.131	0.481 -0.240	0.323 0.354	0.990 0.177	0.471 0.578	
H75632 AA757754	Homo sapiens mRNA for DEC1, complete cds Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds	0.348	0.301	-0.154	-0.023	0.452	0.632	
N73761	Homo sapiens mRNA for dihydropyrimidinase, complete cds	1.818 -0.194	0.863 -0.327	1.662 -0.725	1.674 0.003	0.385 -0.356	-0.464 0.031	
AA757764 AA620421	Homo sapiens mRNA for DNA-binding protein, complete cds Homo sapiens mRNA for doublecortin	0.897	0.082	0.861	0.165	0.613	0.187	
H99695	Homo sapiens mRNA for EDF-1 protein	-0.412 1.061	-0.066 1.099	-0.352 1.396	-0.527 0.491	-0.559 2.248	-0.130 0.682	
AA609284	Nomo sapiens mRNA for Efs1, complete cds Homo sapiens mRNA for Eph-family protein, complete cds	-0.133	0.070	0.142	0.130	0.515	0.965 0.713	
N31585	Homo sapiens mRNA for epiregulin, complete cds Homo sapiens mRNA for ERp26 protein	0.082 -0.025	0.482 -0.033	-0.317 -0.454	-0.489 -0.371	-0.099 -0.297	0.562	
W72051	Homo sapiens mRNA for fatty acid binding protein, complete cds	-0.330	0.065	-0.476	-1.020	-0.019	0.559 -0.085	
N21170	Homo sapiens mRNA for Fln29, complete cds Homo sapiens mRNA for fructose-1,6-bisphosphatase	0.016 0.653	0.103 0.170	0.245 1.006	-0.072 0.084	0.173 0.534	-0.083	
N70841	Homo sapiens mRNA for GABA-BR1a (hGB1a) receptor	-0.241	-0.226	-0.243	-0.718	-0.148 -1.157	0.722 1.144	
AA43410	Homo sapiens mRNA for galectin-9 isoform, complete cds Homo sapiens mRNA for GCP170, complete cds	-1.019 0.002	-1.713 0.079	-1.501 0.234	-1.061 -0.030	0.160	1.172	
R92806	Homo sapiens mRNA for GDP dissociation inhibitor beta	0.311	-0.195	-0.401	0.218	-0.092 -0.363	0.269 0.944	
H88599	Homo sapiens mRNA for GS3786, complete cds	-0.255 -0.193	-0.397 -0.333	-0.181 -0.277	-0.510 -0.197	0.174	0.792	
AA41678	3 Homo sapiens mRNA for GS3955, complete cds 3 Homo sapiens mRNA for H-2K binding factor-2, complete cds	-0.101	0.044	0.188	0.122	0.257	0.659 0.491	
AA45461	Homo sapiens mRNA for Hic-5, partial cds	0.635 0.199	0.638 0.198	0.715 0.303	0.640 1.276	0.844 -0.079	0.273	
N20338 AA42895	Homo sapiens mRNA for Hrs, complete cds Homo sapiens mRNA for HsGAK, complete cds	1.497	0.222	0.657	0.631	0.618	0.646	
AA60851	2 Homo sapiens mRNA for hSNF2h, complete cds	0.024 -0.759	0.665 -0.236	0.494 -0.372	-0.551 -0.109	0.082 -0.566	-0.047 0.691	
AA41962 R01638	8 Homo sapiens mRNA for hTCF-4 Homo sapiens mRNA for HYA22, complete cds	-0.289	-0.199	-0.359	-0.264	-0.355	0.712	
N46828	Homo sapiens mRNA for inositol 1,4,5-trisphosphate 3-kinase isoenzyme, partial cds	-0.309 0.277	-0.049 0.290	-0.698 -0.166	-1.164 -0.268	-0.548 -0.059	0.803 0.874	
H62387	2 Homo sapiens mRNA for interleukin 1 receptor accessory protein, complete cds Homo sapiens mRNA for ISLR, complete cds	0.355	-0.060	-0.390	-0.192	0.137	0.921	
AA67765	5 Homo saniens mRNA for Klotho, complete cds	0.571 0.014	-0.584 -0.010	0.132 -0.188	0.551 -0.325	0.960 -0.175	0.894	
N75028 AA15663	Homo sapiens mRNA for L-3-phosphoserine-phosphatase homologue Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4	0.460	-0.123	0.182	-0.280	0.518	-0.125	
AA70064	7 Homo sapiens mRNA for LECT2 precursor, complete cds	0.442 0.475	0.116 0.300	0.413 0.197	0.475 0.617	0.173 0.054	0.438 0.014	
AA01326	Homo sapiens mRNA for lectin-like oxidized LDL receptor, complete cds Homo sapiens mRNA for leucine zipper bearing kinase, complete cds	0.134	0.628	0.062	0.067	0.339	0.382 0.225	
AA42575	5 Homo sapiens mRNA for leukemia associated gene 1 Homo sapiens mRNA for leukemia associated gene 2	0.440 -0.397	0.355 -0.306	0.068 0.048	-0.040 -0.622	0.325 1.326	0.572	
N25204 AA13319	Homo sapiens mRNA for low molecular mass ubiquinone-binding protein, complete cds	0.032	0.197	0.238	0.187	0.781 2.623	0.433	
AA48622	Homo sapiens mRNA for Lysyl tRNA Synthetase, complete cds	2.042	0.879	1.742	1.106	2.023	U. (= 1	

	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
ACC Gene Name AA046430 Homo sapiens mRNA for membrane glycoprotein gp36	0.215	0.098	0.254	0.331	0.098	0.464	(10) 5255 2 1225
R23752 Homo sapiens mRNA for mitochondrial ribosomal protein S12	-0.094	0.134	0.058	0.351	-0.083	0.674	
AA669126 Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)	0.261	-0.105	-0.733	-0.333	-0.265	0.675	
N91887 Homo sapiens mRNA for NB thymosin beta, complete cds	-0.756	0.136	-0.307	-0.436	-0.557	0.410	
AA625859 Homo sapiens mRNA for Nck, Ash and phospholipase C gamma-binding protein NAP4, partial cds	-0.317	0.271	-0.087	0.210	-0.513	0.078	
R63918 Homo sapiens mRNA for neuronatin alpha, complete cds	1.037	0.858	0.746	0.301	1.323 -0.259	0.172 0.838	
AA186348 Homo sapiens mRNA for neuropathy target esterase	-0.413	-0.313 0.580	0.125 -0.081	-0.105 0.034	0.337	0.690	
AA706226 Homo sapiens mRNA for NTAK, complete cds	0.467 0.332	-0.207	-0.454	0.034	-0.157	0.618	
AA894577 Homo sapiens mRNA for nucleolar protein hNop56	0.128	0.055	0.508	0.199	0.072	0.102	
N52533 Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds AA598653 Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)	-0.142	0.859	-0.512	-0.255	-0.254	-0.205	
N32201 Homo sapiens mRNA for osteomodulin, complete cds	-0.078	0.151	-0.346	-0.093	-0.007	0.371	
AA479199 Homo sapiens mRNA for osteonidogen, complete cds	0.157	0.379	0.382	0.639	0.245	0.838	
AA838730 Homo sapiens mRNA for OTK18, complete cds	0.232	0.139	-0.181	0.141	-0.276	0.638	
AA608583 Homo sapiens mRNA for OTK27, complete cds	-0.264	-0.273	-0.117 0.338	-0.256 -0.006	-0.304 0.350	0.505	
AA504342 Homo sapiens mRNA for p115, complete cds	0.354 -0.538	0.142 -0.429	-0.140	-1.487	-0.530	0.537	•
N91962 Homo sapiens mRNA for p18 component of aminoacyl-tRNA synthetase complex, complete cds	0.789	0.245	0.062	-0.221	0.353	0.804	
AA456077 Homo sapiens mRNA for p27, complete cds	0.197	0.204	-0.117	0.292	0.111	0.697	
AA458622 Homo sapiens mRNA for PCDH7 (BH-Pcdh)a, complete cds AA005153 Homo sapiens mRNA for PDZ domain protein	0.982	0.796	0.645	1.011	0.994	0.346	
T70586 Homo sapiens mRNA for perilipin, complete cds	0.474	0.577	0.158	0.063	0.758	-0.281	
AA446906 Homo sapiens mRNA for peroxisomal integral membrane protein	0.050	-0.031	0.331	0.057	0.312	-0.302	
AA447595 Homo sapiens mRNA for phosphatidylinositol 4-kinase, complete cds	0.159	0.533	-0.209	0.319	-0.108 -0.759	-0.503 0.487	
AA599008 Homo sapiens mRNA for PKU-alpha, partial cds	-0.344	0.243	-0.445 0.896	-0.281 0.601	1.379	0.449	
N26838 Homo sapiens mRNA for polyspecific oraganic cation transporter, complete cds	1.493 -1.249	0.859 -0.170	-0.600	-0.914	-0.542	0.559	
AA485052 Homo sapiens mRNA for proteasome subunit p58, complete cds	0.107	0.586	-0.115	0.745	-0.231	0.809	
H62029 Homo sapiens mRNA for protein kinase, Dyrk3	0.374	-0.281	0.122	0.170	0.276	0.938	
AA465723 Homo sapiens mRNA for protein phosphatase 2C gamma AA679414 Homo sapiens mRNA for PRP8 protein, complete cds	-0.198	0.319	-0.017	0.176	0.543	0.811	
N95462 Homo sapiens mRNA for putative ABC transporter, partial	0.419	0.814	0.146	0.441	0.511	0.648	
AA463411 Homo sapiens mRNA for putative bamacan protein, partial	0.143	-0.067	0.162	-0.074	-0.017	0.223	
AA490159 Homo sapiens mRNA for putative glucose 6-phosphate translocase	0.010	-0.012	0.214	0.413	0.093	0.558 0.891	
AA173926 Homo sapiens mRNA for putative glucosyltransferase, partial cos	-0.274	-0.275	0.075	-0.037 -0.095	-0.140 0.129	-0.237	
AA495949 Homo sapiens mRNA for putative GTP-binding protein	0.753 0.667	0.285 0.842	0.046 0.592	0.574	0.329	0.194	
W72965 Homo sapiens mRNA for putative lipoic acid synthetase, partial	0.228	-0.784	-0.069	0.113	0.118	0.229	
AA047567 Homo sapiens mRNA for putative progesterone binding protein	0.090	0.174	-0.292	-0.041	-0.017	0.367	
AA458563 Homo sapiens mRNA for putative ribulose-5-phosphate-epimerase, partial cds H99843 Homo sapiens mRNA for quinolinate phosphoribosyl transferase, complete cds	0.580	0.338	0.256	0.185	0.781	0.988	
H99843 Homo sapiens mRNA for quinolinate prosphonoosyl transferase, complete cus AA776294 Homo sapiens mRNA for rab geranylgeranyl transferase, alpha-subunit	0.207	0.287	0.226	0.044	0.027	0.958	
H84815 Homo sapiens mRNA for Rab9 effector p40, complete cds	1.400	0.949	1.181	1.940	1.173	0.848	
AA453404 Homo sapiens mRNA for RB18A protein	0.186	0.029	0.046	0.002	-0.118 -0.273	0.714	
AA457153 Homo sapiens mRNA for repressor protein, partial cds	0.132	-0.001	0.061 -0.088	-0.060 0.228	-0.273	0.400	
AA029578 Homo sapiens mRNA for Rer1 protein	0.448 0.413	0.074 0.583	0.153	1.179	0.199	-0.245	
AA668470 Homo sapiens mRNA for RGS5, complete cds	0.137	0.912	-0.251	-0.228	-0.121	-0.541	
N45123 Homo sapiens mRNA for ryanodine receptor 3, complete CDS AA074222 Homo sapiens mRNA for SART-1, complete cds	-0.763	-0.400	-0.254	-0.461	-0.710	-0.542	
AA609655 Homo sapiens mRNA for SCP-1, complete cds	-0.447	0.043	-0.111	-0.537	-0.467	0.309	
AA732873 Homo sapiens mRNA for serine/threonine protein kinase SAK	-0.315	-0.023	-0.139	-0.143	-0.221	0.274	
R48132 Homo sapiens mRNA for SH3 binding protein, complete cds, clone:RES4-23A	-0.890	-0.023	-0.907	-1.551	-1.041	1.040	
R01170 Homo sapiens mRNA for SKAP55 protein	-0.545	-0.328	-0.296 0.487	-0.115 0.434	-0.171 -0.039	0.645 0.861	
AA035384 Homo sapiens mRNA for small subunit of cytochrome b in succinate dehydrogenase complex, complet	-0.152	0.336 0.087	-0.040	-0.110	0.104	0.764	
AA629862 Homo sapiens mRNA for smallest subunit of ubiquinol-cytochrome c reductase, complete cds	0.053 1.125	0.727	0.398	0.358	0.696	0.061	
AA449234 Homo sapiens mRNA for smoothelin AA704255 Homo Sapiens mRNA for spinocerebellar ataxia 7	0.956	0.354	0.838	0.360	0.848	0.728	
	-0.320	-0.198	-0.028	0.162	-0.351	-0.411	
R35231 Homo sapiens mRNA for SPOP R01118 Homo sapiens mRNA for squalene epoxidase, complete cds	0.157	0.280	0.428	0.210	0.185	-0.033	
AA137031 Homo sapiens mRNA for STAT induced STAT inhibitor-2, complete cds	0.192	0.340	0.224	0.470	0.171	0.022	
AA001219 Homo sapiens mRNA for STAT induced STAT inhibitor-3, complete cds	0.502	0.558	0.164	0.122 0.640	0.786 -0.322	0.136 0.433	
AA489785 Homo sapiens mRNA for steroid receptor coactivator 1a	-0.172	0.129 0.932	0.167 -0.085	0.040	0.406	1.197	
AA007632 Homo sapiens mRNA for synaptogyrin 1a	0.741 1.787	0.932	0.883	0.971	1.676	0.825	
N46419 Homo sapiens mRNA for synaptogynin 3	-0.759	-0.125	-0.786	-0.724	-0.581	0.641	
H49443 Homo sapiens mRNA for synaptopodin AA460969 Homo sapiens mRNA for TGF-beta activated kinase 1a, complete cds	0.115	0.239	0.071	-0.001	0.422	0.650	
AA450062 Homo sapiens mRNA for TGF-beta superfamily protein, complete cds	0.183	0.278	0.252	0.036	0.472	0.676	
AA102634 Homo sapiens mRNA for TRAF5, complete cds	0.041	-0.074	0.140	0.078	0.004	0.061	
AA486067 Homo sapiens mRNA for transducin (beta) like 1 protein	0.443	-0.101 0.859	0.543 2.251	0.209 0.936	-0.107 0.845	-0.083 -0.294	
N72715 Homo sapiens mRNA for translational inhibitor protein p14.5	2.805 0.683	0.859	0.448	0.456	0.825	0.315	
AA465355 Homo sapiens mRNA for U3 snoRNP associated 55 kDa protein	0.169	0.101	-0.235	-0.074	-0.265	0.508	
AA424578 Homo sapiens mRNA for UDP-Gal:GlcNAc galactosyltransferase AA486112 Homo sapiens mRNA for vacuolar proton-ATPase subunit M9.2	-0.187	0.044	0.508	0.237	0.289	0.738	
H56595 Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)	0.279	0.067	0.213	0.806	-0.095	1.123	
H51419 Homo sapiens mRNA for voltage gated potassium channel	3.394	0.466	1.151	1.570	1.735	0.978	
AA112979 Homo sapiens mRNA for VRK1, complete cds	-0.073	-0.040	0.247	-0.068 0.551	0.198 0.546	0.975	
AA490617 Homo sapiens mRNA for VRK2, complete cds	0.839	-0.020	0.634 0.655	0.191	0.625	1.344	
R01991 Homo sapiens mRNA for zinc finger protein	0.146	-0.148	0.376	-0.073	0.694	1.168	
AA421783 Homo sapiens mRNA for zinc finger protein FPM315, complete cds H17943 Homo sapiens mRNA for zinc finger protein, complete cds, clone:RES4-26	-0.061	-0.118	-0.053	0.368	0.000	1.293	
AA496887 Homo sapiens MTG8-like protein (MTGR1) mRNA, complete cds	0.028	-0.032	-0.150	0.187	0.017	0.480	
AA127685 Homo sapiens multispanning membrane protein mRNA, complete cds	0.352	1.410	0.037	0.155	0.089	0.366	
AA416685 Homo sapiens Munc13 mRNA, complete cds	-0.237	-0.340	-0.112	-0.434	-0.020	0.634	
AA621155 Homo sapiens MutS homolog (MSH5) mRNA, complete cds	-0.297 0.368	-0.100 0.037	-0.005 0.274	0.347 1.482	-0.095 -0.142	0.760	
R42685 Homo sapiens myo-inositol monophosphatase 2 mRNA, complete cds	0.361	0.037	0.052	0.029	0.197	0.326	
AA157261 Homo sapiens N-acetylglucosamyl transferase component Gpi1 (GPI1) mRNA, complete cds	0.104	-0.023	0.413	-0.022	0.196	0.345	
AA448959 Horno sapiens NADH: ubiquinone oxidoreductase 15 kDa IP subunit mRNA, nuclear gene encoding mit AA055102 Horno sapiens NADH: ubiquinone oxidoreductase 18 kDa IP subunit mRNA, nuclear gene encoding mit	0.228	0.566	-0.088	0.038	0.600	0.884	
AA460251 Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-KFYI mRNA, complete cds	-0.276	-0.015	0.244	0.214	0.174	0.768	
N93053 Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH mRNA, complete cds	0.910	1.039	0.501	0.873	0.947	0.420	
AA402891 Homo sapiens NBMPR-insensitive nucleoside transporter et (ENT2) mRNA, complete cds	-0.289	-0.023	-0.148 -0.007	-0.197 1.068	-0.087 0.721	0.089	
AA400187 Homo sapiens nephrocystin (NPHP1) mRNA, partial cds	0.938 0.280	0.526 0.177	0.380	0.531	0.464	2.493	
R40400 Homo sapiens neural cell adhesion molecule (CALL) mRNA, complete cds	-0.156	-0.170	0.555	-0.237	1.036	-0.003	
W40336 Homo sapiens neuroendocrine-specific protein A (NSP) mRNA, complete cds AA482508 Homo sapiens neuronal apoptosis inhibitory protein mRNA, complete cds	-0.187	-0.382	-0.755	-0.513	0.159	0.690	
AA482508 Homo sapiens neuronal apoptosis limitatory protein (NAP-22) mRNA, complete cds	-0.194	0.100	0.229	-0.167	-0.368	0.658	
AA098867 Homo sapiens neuropilin mRNA, complete cds	0.059	0.208	0.050	0.321	-0.125	0.738	
N26125 Homo sapiens neuropilin-2(a17) mRNA, complete cds	-0.518	1.576	-0.751	-0.577	-0.474	0.675	
AA394127 Homo sapiens NF-AT3 mRNA, complete cds	0.421	0.492	0.158	0.148 -0.093	0.728 0.557	0.691 0.478	
H58953 Homo sapiens NF-E2 protein (NF-E2) mRNA, complete cds	0.092	0.386 -0.320	-0.132 0.247	0.093	0.087	0.591	
H50114 Homo sapiens NMDA receptor mRNA, complete cds	0.143 -0.555	-0.536	-0.549	-0.607	-0.227	0.622	
AA279762 Homo sapiens Nmi mRNA, complete cds T63511 Homo sapiens Notch3 (NOTCH3) mRNA, complete cds	0.372	0.554	-0.303	0.247	0.168	-0.161	
T63511 Homo sapiens Notch3 (NOTCH3) mRNA, complete cos AA055440 Homo sapiens novel antagonist of FGF signaling (sprouty-1) mRNA, partial cds	-0.658	0.318	-0.495	-0.791	-0.161	-0.562	
AA630302 Homo sapiens NRD convertase mRNA, complete cds	0.629	0.580	-0.697	0.311	0.310	0.235	
N71003 Homo sapiens nuclear antigen H731-like protein mRNA, complete cds	0.828	1.049	0.585	0.414	0.933	0.604	
AA418821 Homo sapiens nuclear autoantigen GS2NA mRNA, complete cds	0.715	1.432	-0.199 1.126	0.212 1.022	0.103	0.477 0.204	
H72030 Homo sapiens nuclear domain 10 protein (ndp52) mRNA, complete cds	1.158 1.680	0.187 0.795	2.088	0.387	1.386	0.385	
AA282301 Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds	1.000	0.760	2.000	5.501			

ACC Gene Name		ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
W90085 Homo sapiens nucle	ear hormone receptor (shp) gene, 3' end of cds ear VCP-like protein NVLp.2 (NVL.2) mRNA, complete cds	0.147 0.277	-0.176 0.093	0.191 0.191	-0.147 0.304	0.097 0.249	0.371 0.630	
AA491224 Homo sapiens nucle	ar-encoded mitochondrial cytochrome c oxidase Va subunit mRNA, complete cos	0.308	0.752	-0.024	0.384	0.218 -0.022	0.312	
W81191 Homo sapiens nucle	eolar autoantigen No55 mRNA, complete cds eolar protein (MSP58) mRNA, complete cds	0.019 -0.167	-0.383 -0.334	0.228 -0.284	-0.472	-0.232	0.166	
AA443098 Homo sapiens Opa-	interacting protein OIP2 mRNA, partial cds	0.271 -0.054	0.332	0.490 -0.168	0.382 0.059	0.368 0.236	0.396 0.575	
H54393 Homo sapiens Opa- R55705 Homo sapiens orexi	interacting protein OIP5 mRNA, partial cds n receptor-1 mRNA, complete cds	0.154	0.138	-0.317	-0.325	-0.029	0.564	
W86471 Homo sapiens orexi	n receptor-2 mRNA, complete cds	-1.018 0.179	-0.689 0.129	-0.316 0.205	-0.822 0.497	-0.636 0.275	0.593 0.731	
AA430503 Homo sapiens oriP	binding protein (OBP-1) mRNA, 3' end an G protein-coupled receptor (GPR39) mRNA, complete cds	-0.051	-0.133	0.166	0.064	0.115	0.573	
AA425685 Homo sapiens orph	an nuclear hormone receptor BD73 mRNA, 3' end	0.663 -0.113	0.698 -0.080	0.420 0.465	0.578 0.190	0.588 0.304	0.168 -0.450	
AA400408 Homo sapiens outer R60723 Homo sapiens P2x	r dense fiber protein 2 (odf2) mRNA, complete cds purinoceptor mRNA, complete cds	0.237	0.346	-0.077	-0.072	0.553	-0.115	
R31521 Homo sapiens P52r	IPK mRNA, complete cds	1.184 -0.067	0.490 -0.247	1.855 0.316	0.908 -0.369	0.591 -0.185	-0.352 0.233	
AA683321 Homo sapiens PAR AA446028 Homo sapiens para	-5 mRNA, probable 5' end oxonase (PON2) mRNA, complete cds	0.376	0.600	0.194	0.609	0.180	0.198	
T57069 Homo sapiens para	oxonase 3 (PON3) mRNA, 3' end of cds	-0.060 0.666	0.132 0.314	-0.126 0.191	-0.008 -0.155	-0.097 0.868	0.361 0.647	
R02189 Homo sapiens pero	11p homolog mRNA, complete cds xisomal membrane protein 69 (PMP69) mRNA, complete cds	0.247	0.395	0.034	0.281	0.013	0.424	
M63845 Homo sapiens pero	xisomal phytanoyl-CoA alpha-hydroxylase (PAHX) mRNA, complete cds xisome biogenesis disorder protein 1 (PEX1) mRNA, complete cds	0.042 0.592	0.185 0.780	0.091 0.102	0.189 0.311	0.051 0.298	0.327 -0.411	
R37665 Homo sapiens peso	adillo mRNA, complete cds	0.155	0.205	0.509	0.359	0.411	-0.445 0.073	
AA682855 Homo sapiens PHD	Finger 1 (PHF1) mRNA, complete cds lylalanine hydroxylase (PAH) mutant Q20stop mRNA	0.045 -0.099	-0.081 -0.239	0.288 0.109	-0.208 0.188	0.189 -0.119	0.055	
R59165 Homo sapiens phos	phatase 2A B56-alpha (PP2A) mRNA, complete cds	-0.112	-0.048	0.068	0.404 -0.069	-0.045 0.220	0.005 0.251	
R40460 Homo sapiens phos	phatidylinosito! 4-kinase mRNA, complete cds phatidylinosito! 4-kinase mRNA, complete cds	-0.033 -0.021	0.093 -0.059	0.129 0.040	-0.061	0.055	0.511	
A A 420E20 Home envione phos	photidulinosital synthase (PIS) mRNA, complete cds	-0.040	-0.258	0.294 0.231	0.164 -0.033	-0.183 -0.238	0.268	
	phodiesterase I/nucleotide pyrophosphatase beta (PDNP3) mRNA, complete cds phoglucomutase-related protein (PGMRP) gene, complete cds	-0.118 -0.191	-0.082 -0.316	0.056	0.192	-0.220	0.012	
AA418524 Homo sapiens phos	pholipase D2 (PLD2) mRNA, complete cds .	1.048	0.457	0.209 0.165	0.026 0.136	0.131 -0.161	0.215	
N25945 Homo sapiens phos	pholipid scramblase mRNA, complete cds phomevalonate kinase mRNA, complete cds	0.208 -0.014	0.044 -0.316	0.022	0.148	-0.358	0.336	
AA100036 Homo sapiens Pig1	0 (PIG10) mRNA, complete cds	0.252	0.396	0.636 0.687	0.863 0.341	0.874 1.726	0.032 -0.046	
	1 (PIG11) mRNA, complete cds 2 (PIG12) mRNA, complete cds	1.190 -0.298	0.824 -0.102	0.125	0.001	-0.348	-0.532	
AA668595 Homo sapiens Pig3	(PIG3) mRNA, complete cds	0.378	-0.074 -0.303	0.008 0.078	0.053 -0.167	0.535 -0.250	0.187 0.151	
AA625666 Homo sapiens Pig7 AA702548 Homo sapiens Pig8	(PIG7) mRNA, complete cds (PIG8) mRNA, complete cds	0.055 -0.369	-0.153	-0.193	0.263	-0.313	0.370	
AA732983 Homo sapiens PIG	CP1 pseudogene	-0.345 0.264	-0.035 -0.350	0.012 -0.102	-0.109 -0.396	0.348 -0.189	0.047 -0.190	
AA458849 Homo sapiens plac N64508 Homo sapiens pode	ental bikunin mRNA, complete cds ocalyxin-like protein mRNA, complete cds	0.181	0.484	0.078	-0.220	-0.043	-0.104	•
AA040742 Homo sapiens poly	(A) binding protein II (PABP2) gene, complete cds	0.915 0.103	0.313 0.115	0.369	0.869 0.298	-0.265 0.560	-0.068 0.021	
AA700904 Homo sapiens Porc	ADP-ribose) glycohydrolase (hPARG) mRNA, complete cds -Pl gene similar to yeast CDC45	-0.446	-0.371	-0.102	0.014	-0.278	0.149	
R39954 Homo sapiens post	-synaptic density protein 95 (PSD95) mRNA, complete cds	-0.084 0.538	-0.048 0.758	0.058	-0.281 0.285	-0.166 0.487	-0.122 -0.315	
H08545 Homo sapiens pota AA069770 Homo sapiens pota	ssium channel homolog (KCNQ3) mRNA, partial cds ssium channel Kv2.1 mRNA, complete cds	0.466	-0.212	0.151	-0.143	0.169	-0.544	
N99154 Homo sapiens PRK	Y exon 1 and joined CDS	0.122 -0.164	0.268 0.068	-0.916 -0.421	-0.271 -0.235	-0.603 -0.142	-0.841 -0.245	
AA430552 Homo sapiens profi	ne-rich Gla protein 1 (PRGP1) mRNA, complete cds ne-rich Gla protein 2 (PRGP2) mRNA, complete cds	0.001	-0.638	-0.133	-0.148	-0.393	-1.448 -0.622	
AA037014 Homo sapiens pros	taglandin transporter hPGT mRNA, complete cds	0.542 -0.486	0.171 -0.112	0.315 -0.377	0.865 -0.272	-0.134 0.003	-0.182	
AA872020 Homo sapiens pros AA863149 Homo sapiens prot	easome subunit XAPC7 mRNA, complete cds	0.036	-0.406	0.305	-0.071 0.542	0.078 0.217	-0.536 -0.209	
AA449738 Homo sapiens prot	ein 4.1-G mRNA, complete cds ein H5 (H5) mRNA, complete cds	0.112 0.240	0.417 0.191	-0.139 -0.093	0.271	0.397	0.064	
AA071486 Homo sapiens prot	ein kinase mRNA, complete cds	0.300	0.151 0.350	0.106 0.300	0.279 0.324	0.137 0.069	0.563 -0.529	
AA129171 Homo sapiens prot R53787 Homo sapiens prot	ein phosphatase 2A B56-beta (PP2A) mRNA, complete cds ein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds	0.543 -0.169	0.378	0.045	0.167	0.824	-0.175	
N33955 Homo sapiens prot	ein phosphatase Wip1 mRNA, complete cds	0.502 0.384	0.430 0.227	0.093 0.017	0.043 0.105	0.368 0.498	-0.392 0.235	
H18855 Homo sapiens prot	ein phosphatase with EF-hands-1 (PPEF-1) mRNA, complete cds ein regulating cytokinesis 1 (PRC1) mRNA, complete cds	0.044	0.226	-0.223	0.759	0.020	-0.582	
R59598 Homo sapiens prot	ein tyrosine kinase (Syk) mRNA, complete cds	0.141 0.697	0.032 0.507	0.205 0.412	0.086 -0.029	0.481 0.706	-0.441 0.070	
W72792 Homo sapiens prot	ein tyrosine kinase (Syk) mRNA, complete cds ein-tyrosine kinase EPHB2v (EPHB2) mRNA, complete cds	-0.031	0.412	0.332	0.465	0.535	0.132	
NO0793 Homo conjens nuri	nergic receptor P2Y5 mRNA, complete cds utive ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear gene end	-0.134 c 0.746	-0.141 0.279	-0.394 0.289	-0.292 0.694	-0.307 0.948	0.227	
P05733 Homo caniens nuts	itive DNA methyltransferase (DNMT2) mKNA, complete cos	0.522	0.424	-0.028	-0.387 -0.202	0.463 0.272	0.142 0.571	
W49667 Homo sapiens puta	tive fatty acid desaturase MLD mRNA, complete cds tive glycine-N-acyltransferase mRNA, complete cds	0.119 0.431	0.152 0.301	-0.081 0.389	0.056	0.332	0.201	
R69593 Homo sapiens puta	itive monocarboxylate transporter MCT mRNA, complete cds	0.621	-0.431 0.087	1.048 0.615	1.421 0.296	0.703 0.027	-0.772 -0.478	
AA610004 Homo sapiens puta	ntive oncogene protein mRNA, partial cds ntive oral tumor suppressor protein (doc-1) mRNA, complete cds	0.013 0.312	0.460	0.427	0.255	0.351	0.571	
AAAE7720 Homo eaniene ruits	itive OSP like nrotein mRNA, partial cds	0.024 -0.386	-0.149 0.140	0.124 -0.462	-0.509 -0.610	-0.109 -0.389	-0.288 -0.160	
AAE20070 Homo conjent built	ative RNA binding protein KOC (koc) mRNA, complete cds ative seven pass transmembrane protein (TM7SF1) mRNA, complete cds	0.331	0.173	0.399	0.480	0.202	0.233	
W84524 Homo sapiens put	ative tetraspan transmembrane protein L6H (TM4SF5) mKNA, complete cos	0.599 0.421	0.574 -0.017	0.309 0.209	0.359 0.454	0.575 0.032	-0.029 0.280	
AAA54050 Homo saniens nut:	ative transcription factor CA150 mRNA, complete cds ative tumor suppressor protein (101F6) mRNA, complete cds	1.430	0.382	0.788	0.840	0.345	0.213	
DAA982 Home saniers nut:	ative tumor suppressor protein unspliced form (Fus-2) micha, complete cus	-0.023 0.219	0.367 0.007	0.513 -1.112	0.295 -1.152	0.224 -0.669	0.727 -0.015	
H29475 Homo sapiens pyri N63567 Homo sapiens pyri	zvate dehydrogenase kinase isoenzyme 2 (PDK2) mRNA, complete cds zvate dehydrogenase kinase isoenzyme 3 (PDK3) mRNA, complete cds	0.205	-0.218	-0.327	-0.261	-0.322	-0.388	
AA464152 Homo sapiens quie	escin (Q6) mRNA, complete cds	-0.378 0.533	-0.256 0.522	-0.323 0.033	-0.157 0.178	-0.127 0.161	-0.121 -0.269	
N51095 Homo sapiens Rac T64150 Homo sapiens Rac	3 (RAC3) mRNA, complete cds 151C (RAD51C) mRNA, complete cds	0.290	0.790	-0.045	0.410	-0.077	-0.142 -0.043	
N29765 Homo sapiens RA	DS1D mRNA, complete cds BP1-interacting protein (POB1) mRNA, complete cds	-0.160 0.863	-0.207 0.697	0.091 0.114	-0.139 0.209	0.019 0.844	0.227	
AA430178 Homo sapiens Rar	binding protein 2 (RanBP2alpha) mRNA, partial cds	0.918	1.248	0.928	0.323	0.936 -0.437	0.059 -1.139	
R11189 Homo sapiens RA	NBP8 mRNA, complete cds P2 interacting protein 8 (RPIP8) mRNA, complete cds	-0.155 -0.316	-0.084 -0.287	-0.414 -0.797	-0.114 -1.060	-0.437	0.142	
AA422006 Homo espient PC	(Rci) mRNA complete cds	-0.071	0.331	-0.292 -1.180	-0.313 -0.763	0.403 -0.498	0.191 -0.307	
H70047 Homo sapiens reg	ulator of G protein signaling (RGS13) mRNA, complete cds	0.082 -0.052	0.492 0.075	0.419	0.556	-0:050	-0.081	
AA158244 Homo sapiens req	ulator of G protein signaling KGS12 (KGS) mKNA, complete cus	0.267	0.301 0.895	0.529 0.634	0.399 0.246	0.111 1.068	0.196 -1.043	
W72679 Homo sapiens reti	noblastoma-associated protein HEC mRNA, complete cds noic acid hydroxylase mRNA, complete cds	0.508 0.255	0.303	-0.261	0.702	0.088	-0.053	
T41177 Homo sapiens reti	noic acid-inducible endogenous retroviral DNA	0.178 -0.032	0.047 0.446	0.377 -0.088	0.150 0.861	0.474 -0.471	0.282 -0.016	
AA405000 Homo sapiens ribo	onuclease 6 precursor, mRNA, complete cds ui (RIGUI) mRNA, complete cds	-0.050	-0.031	0.429	0.613	0.030	-0.029	
AA598640 Homo sapiens ring	i finger protein (FXY) mRNA, complete cds	0.022 -0.087	-0.105 0.031	1.250 0.130	-0.061 0.195	0.147 0.223	0.382 -0.284	
AA733038 Homo saniens RN	G zinc finger protein (RZF) mRNA, complete cds A polymerase I subunit hRPA39 mRNA, complete cds	-0.223	-0.082	-0.234	-0.225	0.198	0.005	
MR4896 Homo panione RN	A notymerase il elongation factor SIII, D15 suburit micha, complete cos	0.269 -0.298	0.450 -0.175	-0.243 -0.685	-0.075 -0.647	0.166 -0.327	0.085 -0.241	
AA630017 Homo sapiens RN AA777406 Homo sapiens rou	A polymerase II transcription factor SIII p18 subunit mRNA, complete cds indabout 1 (robo1) mRNA, complete cds	-0.456	-0.020	-0.022	-0.149	0.043	0.131	

ACC Gene Name	ZR75 0.918	YY3 0.287	YY1 0.593	468 -0.412	MPI -0.822	231 -0.117	(log base 2 ratio
AA186327 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds AA620859 Homo sapiens sarcospan-2 (SPN2) mRNA, complete cds	-0.117	-0.434	-0.224	-0.471	-0.187	-0.454	
T68892 Homo sapiens secreted frizzled related protein mRNA, complete cds	0.173	0.547	-0.404	-0.032 -1.790	-0.172 -0.792	-0.148 0.150	
AA430443 Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds R72518 Homo sapiens secretory carrier membrane protein (SCAMP3) mRNA, complete cds	-1.245 0.493	-0.588 0.097	-1.487 0.379	0.098	0.396	0.058	
AA490945 Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds	0.057	0.188	-0.006	0.186	0.557	-0.059 0.222	
AA436152 Homo sapiens semaphorin F homolog mRNA, complete cds	0.284 0.470	0.266 0.487	0.164 0.198	0.602 0.410	0.404 0.586	0.222	
T65211 Homo sapiens serine kinase SRPK2 mRNA, complete cds AA459401 Homo sapiens serine protease-like protease (nes1) mRNA, complete cds	0.355	-0.091	0.173	-0.265	1.061	0.499	
AA282196 Homo sapiens serine/threonine protein kinase mRNA, complete cds	0.219	0.476	0.319	0.276 -0.222	0.065 -0.031	0.453 0.917	
AA486082 Homo sapiens sgk gene	0.297 -0.182	0.064 -0.108	0.031 0.111	0.058	0.269	0.254	
AA700222 Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds AA455640 Homo sapiens signalosome subunit 3 (Sgn3) mRNA, complete cds	-0.037	-0.119	-0.085	-0.286	0.530	0.211	
R18237 Homo sapiens sin3 associated polypeptide p18 (SAP18) mRNA, complete cds	0.369 0.024	0.069 -0.223	0.306 -0.515	-0.121 -0.736	0.328 -0.149	0.265 -0.015	
AA496357 Homo sapiens SKB1Hs mRNA, complete cds AA455925 Homo sapiens skeletal muscle LIM-protein FHL1 mRNA, complete cds	0.431	0.095	0.219	0.593	-0.190	0.309	
AA460438 Homo sapiens skeletal muscle LIM-protein FHL3 mRNA, complete cds	0.167	0.063	0.075	0.751 0.618	-0.168 0.657	-0.156 -1.107	
AA424700 Homo sapiens SMAD5 (Smad5) mRNA, complete cds	1.323 -0.508	0.621 -0.621	1.224 -0.644	-1.184	-0.558	0.102	
AA628430 Homo sapiens Sm-like protein CaSm (CaSm) mRNA, complete cds AA452278 Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds	0.463	0.752	-0.029	0.228	0.238	0.049	
AA490044 Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cos	0.959 -0.726	0.510 -0.619	0.717 -0.721	0.724 -0.659	1.011 -0.540	0.151 0.091	
AA171463 Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds AA428551 Homo sapiens SOX22 protein (SOX22) mRNA, complete cds	0.091	0.097	-0.049	-0.327	-0.074	0.395	
N54552 Home sapiens spindle pole body protein spc98 homolog mRNA, complete cds	0.234	0.182	-0.009 0.242	0.270 0.217	-0.029 0.404	-0.401 0.207	
AA449693 Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA, complete cds H47069 Homo sapiens splicing factor (CC1.3) mRNA, complete cds	-0.447 0.632	0.178 0.219	0.264	0.154	0.326	0.220	
H78241 Homo sapiens splicing factor Sip1 mRNA, complete cds	0.116	0.234	0.338	0.247	-0.068	-0.476	
AA453759 Homo sapiens Sprouty 2 (SPRY2) mRNA, complete cds	0.435 0.155	0.147 0.507	0.046 0.724	-0.256 0.762	0.075 0.247	0.030 -0.968	
AA609599 Homo sapiens SSX3 (SSX3) mRNA, complete cds AA085319 Homo sapiens stanniocalcin precursor (STC) mRNA, complete cds	0.021	-0.012	-0.289	0.113	0.129	-0.492	
AA488247 Homo sapiens stat-like protein (Fe65) mRNA, complete cds	-0.027	-0.012	0.136	-0.291	0.182	-0.072 0.067	
AA425401 Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds	-0.390 0.375	-0.405 0.173	-0.853 -0.147	-1.329 -0.119	-0.593 0.359	0.082	
H61188 Homo sapiens Su(var)3-9 homolog (SUV39H) mRNA, complete cds T57810 Homo sapiens supervillin mRNA, complete cds	0.549	1.355	0.396	0.651	0.371	0.244	
AAA25806 Homo saniens sungressin (spn) mRNA, complete cds	1.728	0.526	0.515	0.433	0.330	0.067 -0.423	
N26026 Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA, complete cos	0.069 0.344	0.090 0.287	0.182 0.118	-0.322 0.187	0.115 0.228	0.107	
H87106 Homo sapiens T245 protein (T245) mRNA, complete cds AA679208 Homo sapiens TAK1 binding protein (TAB1) mRNA, complete cds	0.156	0.068	0.384	-0.171	0.195	0.285	
T69304 Homo sapiens tapasin (NGS-17) mRNA, complete cds	0.227	0.254	0.503	0.774 -0.486	0.470 -0.854	-0.346 -0.169	
AA434159 Homo sapiens Tax interaction protein 2 mRNA, partial cds	-0.187 -0.369	0.228 -0.254	0.238. -0.197	-0.472	-0.393	0.022	
AA757170 Homo sapiens Tax interaction protein 33 mRNA, partial cds AA621019 Homo sapiens Tax interaction protein 40 mRNA, partial cds	1.089	0.582	0.193	0.368	0.420	-0.170	
R10726 Homo sapiens Tax interaction protein 43 mRNA, partial cds	0.537 0.013	0.791 0.082	1.594 0.218	2.572 0.521	0.072 0.246	0.204 0.314	
W85892 Homo sapiens TBP-associated factor 172 (TAF-172) mRNA, complete cds H67086 Homo sapiens TEB4 protein mRNA, complete cds	0.391	0.111	0.153	-0.009	0.455	0.353	
AA151294 Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds	0.654	0.553	0.405	0.352	1.131	0.169	
AA406064 Homo sapiens testis-specific Basic Protein Y 1 (BPY1) mRNA, complete cos	0.455 0.155	0.455 0.030	-0.292 0.052	0.610 0.015	0.454 0.147	-0.391 -1.194	
AA100696 Homo sapiens tetraspan (NAG-2) mRNA, complete cds AA464601 Homo sapiens tetraspanin Tspan-5 (TSPAN-5) gene, complete cds	0.420	1.218	0.213	-0.535	0.592	-0.205	
AA156940 Homo sapiens TFAR19 mRNA, complete cds	0.110	0.819	0.128	-0.132	-0.264 -0.357	-0.125 -0.182	
AA078976 Homo sapiens thioredoxin-like protein mRNA, complete cds	-0.356 0.281	-0.326 0.818	-0.280 0.115	0.289 0.378	-0.357	-0.147	
AA774044 Homo sapiens thrombospondin 3 (THBS3) gene, complete cds AA486239 Homo sapiens thyroid autoantigen (truncated actin-binding protein) mRNA, complete cds	0.667	1.037	0.626	0.921	0.627	0.071	
AA489011 Homo sapiens thyroid receptor interactor (TRIP3) mRNA, 3' end of cos	0.336	0.750	0.383	0.768 0.589	0.090 0.301	0.322 0.473	
AA476490 Homo sapiens thyroid receptor interactor (TRIP4) mRNA, 3' end of cds	0.138 -0.007	0.731 0.524	0.230 0.317	0.446	0.665	0.640	
AA431321 Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds AA806371 Homo sapiens thyroid receptor interactor (TRIP9) gene, complete cds	1.960	-0.085	1.016	0.624	1.832	-0.321	
AA916906 Homo sapiens TNF receptor-1 associated protein (TRADD) mRNA, 3' end of cds	0.472 0.035	0.539 0.118	0.225 0.212	0.271 0.030	0.641 0.704	-0.079 -0.410	
AA485752 Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds AA504211 Homo sapiens TNF-related ligand TRANCE mRNA, partial cds	0.033	0.643	-0.249	-0.160	0.086	-0.402	
AA394148 Homo sapiens torsinA (DYT1) mRNA, complete cds	0.272	0.365	0.101	1.223	0.196	-0.268 -0.672	
AA040879 Homo sapiens torsinB (DQ1) mRNA, partial cds	0.993	0.552 -0.111	0.174 0.156	0.541	0.436 0.299	-0.287	
AA497031 Homo sapiens TPA inducible protein mRNA, complete cds AA453410 Homo sapiens TRAIL receptor 2 mRNA, complete cds	0.189	0.596	0.195	0.038	0.614	0.213	
AA454218 Homo sapiens transcription factor SL1 mRNA, complete cds	-0.095 -0.098	-0.260 0.093	-0.153 0.463	-0.210 0.446	-0.344 0.323	0.242 0.379	
R32478 Homo saplens transcription factor SL1 mRNA, partial cds AA454673 Homo saplens transcription factor ZFM1 isoform B3 mRNA, complete cds	0.084	0.695	0.490	0.818	0.747	0.860	
R39430 Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cos	0.332	0.801	-0.023	0.204	0.386	0.950 -0.833	
H82891 Homo sapiens trans-golgi network glycoprotein 46 (hTGN46) mRNA, complete cas	0.185 0.517	0.331 0.102	-0.152 -0.126	-0.125 -0.191	0.371 -0.131	-0.748	
H94482 Homo sapiens transmembrane protein mRNA, complete cds AA190941 Homo sapiens Trio mRNA, complete cds	0.751	1.056	0.874	0.580	0.064	-0.256	
AA676590 Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds	-0.234	-0.115	-0.296	-0.657 -0.253	-0.154 0.070	-0.860 -0.195	
AA434139 Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds AA857195 Homo sapiens tumor-suppressing subchromosomal transferable fragment 1 (TSSC1) mRNA, complete	-0.467	0.186	-0.139 0.002	0.462	0.385	-0.478	
N35070 Homo sapiens TWEAK mRNA, complete cds	0.242	0.041	0.359	0.541	0.186	-0.527	
T49657 Home saniens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds	0.230 0.754	0.053 0.189	-0.158 -0.382	-0.391 -0.150	-0.178 0.069	-0.532 0.093	
R45941 Homo sapiens tyrosine phosphatase (IA-2/PTP) mRNA, complete cds AA703250 Homo sapiens U4/U6 small nuclear ribonucleoprotein hPrp4 mRNA, complete cds	-0.046	-0.010	-0.094	-0.073	0.116	0.461	
A 5 GR470 Homo saniens U5 snRNP 100 kD protein mRNA, complete cds	-0.039	0.153	0.211	0.425	0.302 -0.152	0.607 0.767	
AA292074 Homo sapiens ubiquitin conjugating enzyme (UbcH8) mRNA, complete cds	0.021 -0.038	0.347 0.368	-0.248 0.243	0.461 -0.039	-0.197	0.349	
AAA43634 Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds H90287 Homo sapiens ubiquitous TPR motif, X isoform (UTX) mRNA, alternative transcript 1, complete cds	0.012	0.390	-0.220	-0.206	-0.024	-0.057	
AA280832 Homo saniens UDP-galactose-4-epimerase (GALE) mRNA, complete cds	0.212	0.537	-0.148	-0.719 -0.045	-0.466 0.238	0.023 -0.098	
AA418410 Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA, complete cds AA088475 Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, co	0.552 -0.586	0.310 -0.003	0.247 -1.043	-0.043	-1.216	-0.942	
AA704511 Homo sapiens vasionessin activated calcium incoming potential receptor (VTI1) mRNA, complete cds	-0.235	0.200	-0.172	0.262	0.381	0.086	
NG4064 Home seniors Werner syndrome gene complete cds	0.442 -0.110	0.609 0.111	0.003 -0.055	-0.166 -0.033	0.463 0.336	-0.068 -0.727	
AA459013 Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds AA115537 Homo sapiens zinc finger protein (ZNF198) mRNA, complete cds	1.267	0.416	0.825	0.741	0.871	-0.195	
AA252169 Home sapiens zinc finger protein mRNA, complete cds	-0.151	0.592	0.351	0.460	0.633 1.484	0.744 0.470	
N59119 Homo sapiens zinc finger transcription factor (ZNF207) mRNA, complete cus	1.843 1.446	0.726 1.525	1.448 2.008	1.331 0.699	1.484	0.899	
AA046525 Homo sapiens, alpha-1 (VI) collagen AA448277 Homolog 1 of Drosophila forkhead (rhabdomyosarcoma)	0.310	1.070	-0.043	-0.259	0.420	0.536	
R60019 Homolog 2 of Drosophila large discs	0.625	0.096	0.227 -0.033	0.155 -0.004	-0.195 0.454	0.027 0.439	
W44685 Homolog 3 of Drosophila large discs	-0.197 0.093	-0.186 0.304	-0.033 -0.118	-0.056	0.347	-0.865	
AA598758 Homologue of mouse tumor rejection antigen gp96 N94487 Homone receptor (growth factor-inducible nuclear protein N10)	0.687	0.585	0.457	0.452	0.977	-0.399	
774142 HPV16 E1 protein binding protein	0.389 1.146	0.920 0.834	0.238 0.150	-0.489 0.262	-0.036 0.470	0.116 0.024	
T74142 HPV16 E1 protein binding protein N63260 HSMP-1	-0.097	-0.096	-1.198	-0.078	0.124	-0.033	
AA446017 HTS1	0.263	0.139	0.214	-0.149	0.215 0.047	0.046 0.689	
AA456008 Human (AF1q) mRNA, complete cds	0.168 0.022	0.138 -0.081	-0.322 -0.374	-0.600 -0.324	-0.389	0.530	
N66208 Human (ard-1) mRNA, complete cds AA496784 Human (chromosome 3p25) membrane protein mRNA	0.319	1.059	0.359	0.851	0.539	0.862	
H53340 Human (clone 14VS) metallothionein-IG (MT1G) gene, complete cds	1.139 -0.021	0.455 0.751	0.938 0.558	0.244 0.433	0.761 0.887	0.453 -0.525	
AA418564 Human (clone 8B1) Br-cadherin mRNA, complete cds	-0.021	3.731	0.000	5.400	2.00.		

		7075	w	YY1	468	MPI	231	(log base 2 rati
	Gene Name	ZR75 0.059	9743 0.906	0.589	0.522	0.379	0.222	(IOS Dase 2 140
AA496879 H	luman (clone E5.1) RNA-binding protein mRNA, complete cds luman (clone N5-4) protein p84 mRNA, complete cds	-0.047	0.599	0.237	0.196	0.052	0.115	
AA201300 F	luman (clone pA3) protein disulfide isomerase related protein (ERp72) mRNA, complete cds	-0.078	0.081	0.399	-0.110	0.103	0.087	
AA424786 H	luman (clone SY11) golgin-95 mRNA, complete cds	-0.108	-0.047	0.341	-0.326	0.959	0.201	
H58873 H	luman (HepG2) glucose transporter gene mRNA, complete cds	0.319	0.544	-0.144	0.165	0.362	0.311	
AA479741 H	luman (Hin-3)/HIV1 promoter region chimeric mRNA, complete cds	-0.102	0.209	-0.370	-0.577 -0.233	0.448 -0.605	0.578 0.061	
N26665 H	luman (lambda) DNA for immunogloblin light chain	-0.899 0.119	1.052 0.004	-1.001 0.387	0.831	-0.166	0.832	
AA669341 H	luman (p23) mRNA, complete cds	-0.687	-0.171	-0.654	-0.892	-0.227	1.023	
	luman 100 kDa coactivator mRNA, complete cds luman 14-3-3 epsilon mRNA, complete cds	-0.078	0.526	-0.105	0.361	0.363	0.751	
N21624 H	luman 150 kDa oxygen-regulated protein ORP150 mRNA, complete cds	0.280	0.019	-0.122	-0.131	0.316	0.470	
AA086038 H	luman 180 kDa transmembrane PLA2 receptor mRNA, complete cds	0.456	0.610	0.373	0.333	0.524	0.933	
AA459100 H	luman 19.8 kDa protein mRNA, complete cds	-0.190	0.127	0.467	0.242	0.566	0.691 -1.017	
AA877166 F	luman 20-kDa myosin light chain (MLC-2) mRNA, complete cds	0.045	0.122	0.344	0.218 -0.469	0.349 0.254	-0.350	
R08876 F	luman 26S proteasome-associated pad1 homolog (POH1) mRNA, complete cds	-0.540 -0.540	0.105 0.044	-0.212 -0.242	-0.451	0.212	-0.050	
AA400893 F	luman 3',5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA, complete cds	0.655	0.745	0.248	0.727	0.055	0.037	
AA521228 F	tuman 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds tuman 44.9 kDa protein C18B11 homolog gene, partial cds	0.041	0.349	0.092	0.388	0.074	0.221	
R32439 F T39411 F	tuman 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds	0.076	0.615	0.949	1.209	0.421	0.190	
W86653 H	luman 54 kDa progesterone receptor-associated immunophilin FKBP54 mRNA, partial cds	0.618	0.793	0.184	0.566	0.171	0.490	
AA056465 H	luman 54 kDa protein mRNA, complete cds	-0.243	-0.221	-0.157	-0.303	-0.210 -0.246	0.853 0.634	
AA070495 H	luman 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds	0.229 -0.249	0.164 0.356	0.459 0.135	0.399 0.535	-0.410	0.743	
AA010352 F	Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds	0.356	0.017	0.247	0.787	-0.179	0.428	
N64014 F	luman 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha mRNA, clone PIP5KIa1. comple luman 76 kDa tyrosine phosphoprotein SLP-76 mRNA, complete cds	0.436	-0.524	-0.232	0.216	-0.353	0.564	
N52958 F R44334 F	tuman 90 kD heat shock protein gene, complete cds	0.486	1.114	0.436	-0.016	0.539	-0.424	
R44334 H	tuman 90 kD heat shock protein gene, complete cds	0.668	0.790	0.060	0.104	0.542	-0.307	
AA453774 F	luman A28-RGS14p mRNA, complete cds	0.042	0.126	0.613	0.495	0.036	-0.351	
AA055811 F	Human A33 antigen precursor mRNA, complete cds	0.285	-0.124	0.316	0.323	-0.020 -0.108	0.159 0.224	
AA451935 F	Human Aac11 (aac11) mRNA, complete cds	-0.134 1.334	-0.199 1.130	-0.285 0.281	-0.170 0.319	0.493	0.164	
T71209 F	Human abnormal beta-hexosaminidase alpha chain (HEXA) mRNA, partial cds	-0.204	-0.048	-0.186	0.219	-0.300	0.646	
AA451741 F	Human acetolactate synthase homolog mRNA, complete cds	0.160	0.463	-0.499	0.017	-0.653	0.759	
AA/72810 F	Human acidic 82 kDa protein mRNA, complete cds Human activated p21cdc42Hs kinase (ack) mRNA, complete cds	0.072	-0.199	-0.105	-0.148	0.146	0.694	
AA035455 F	-tuman acvi-CoA thioester hydrolase mRNA, complete cds	0.468	0.295	0.275	0.165	0.248	0.477	
AA045508 H	-tuman adenylyl cyclase-associated protein homolog CAP2 (CAP2) mRNA, complete cds	0.608	0.235	0.540	0.686	0.446	0.245	
R61295 H	Human ADP/ATP translocase mRNA, 3' end, clone pHA18	0.526	0.513 0.797	-0.083 -0.511	-0.274 -0.864	0.078 -0.008	0.268 -0.316	
	Human ADP/ATP translocase mRNA, 3' end, clone pHAT8	0.698 -0.331	0.797	0.021	0.294	-0.161	-0.081	
H11049	Human ADP-ribosylation factor 1 (ARF1) mRNA, complete cds	0.640	0.725	0.218	0.343	0.322	0.242	
H11049 H	Human ADP-ribosylation factor 1 (ARF1) mRNA, complete cds Human ADP-ribosylation factor mRNA, complete cds	-0.367	-0.260	0.097	0.438	-0.173	0.237	
H28952 H	Human ADP-ribosylation factor mRNA, complete cds	0.128	0.389	0.337	-0.111	0.226	0.219	
AA779165 H	Human ADP-ribosylation factor-like protein 4 mRNA, complete cds	-0.501	-0.227	0.126	-0.398	-0.247	0.380	
AA284856 H	Human adult heart mRNA for neutral calponin, complete cds	-0.020	0.030	-0.157	-0.266	-0.185	0.758 0.612	
N26539 F	Human AF-6 mRNA complete cds	1.553 -0.997	-1.607 0.224	1.097 -0.066	1.104 -0.995	-1.057 0.209	0.677	
N59115 F	Human alpha1-fetoprotein transcription factor (hFTF) mRNA, complete cds	1.007	0.292	0.469	0.271	0.441	0.663	
AA633747 H	Human alpha-2 collagen type VI mRNA, 3' end Human alpha2,8-sialyltransferase mRNA, complete cds	-0.031	0.323	-0.104	0.385	-0.197	0.433	
R43753 H	Human alpha-2-macroglobulin mRNA, complete cds	0.406	0.144	0.559	-0.030	-0.230	-0.089	
H06516	Human alpha-2-macroglobulin mRNA, complete cds	0.154	0.347	0.212	0.336	-0.225	0.156	
N90109	Human alpha-cardiac actin gene, 5' flank and	0.432	0.071	0.160	-0.082	0.203 -0.342	-0.054 0.141	
AA490047 F	Human alpha-CP1 mRNA, complete cds	0.246 0.122	0.567 -0.168	0.447 0.218	0.444 0.125	0.354	0.161	
AA626698 I	Human alpha-tubulin isotype H2-alpha gene, last exon	2.299	1.325	1.643	0.184	0.869	0.445	
AA865469 P	Human alpha-tubulin mRNA, 3' end Human AMP deaminase (AMPD2) mRNA	-0.074	-0.010	0.198	0.198	0.088	0.318	
R40634 H	Human AMP deaminase (AMPD2) mRNA	0.107	0.165	0.305	-0.080	-0.002	-0.946	
AA126860 H	Human amyloid precursor protein-binding protein 1 mRNA, complete cds	0.054	-0.437	0.123	-0.209	-0.055	0.496	
N62866	Human amyloid precursor-like protein 1 mRNA, complete cds	0.444	0.152	0.259	0.284	0.706 0.282	0.167 -0.478	
AA609880 H	Human anion exchanger 3 brain isoform (bAE3) mRNA, complete cds	0.121 0.358	-0.206 0.040	-0.350 0.447	0.168 -0.045	0.154	-0.335	
AA609759	Human antimicrobial LPS-binding protein CAP18 precursor mRNA, complete cds	0.325	-0.828	0.394	0.261	0.226	0.057	
AA459663	Human antioxidant enzyme AOE37-2 mRNA, complete cds Human antisecretory factor-1 mRNA, complete cds	0.345	-1.675	-0.058	0.355	0.584	-0.191	
AA630778 I	Human AP-3 complex delta subunit mRNA, complete cds	0.257	-0.712	-0.441	0.245	-0.396	-0.139	
R43778	Human APEG-1 mRNA, complete cds	0.097	0.022	0.113	-0.027	-0.002	0.320	
H45618	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor), complete cds	-0.262	0.150	0.155	0.420 0.643	0.128 0.161	0.249 -0.406	
H80712	Human apoptotic cysteine protease Mch4 (Mch4) mRNA, complete cds	0.917 0.449	0.026 0.528	0.583 0.229	0.347	0.086	-0.739	
AA598510 I	Human APRT gene for adenine phosphoribosyltransferase Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD1) mRNA, complete cds	0.337	0.479	0.266	0.500	-0.099	-0.350	
AA625014 1	Human arfaptin 2, putative target protein of ADP-ribosylation factor, mRNA, complete cds	-0.304	0.110	-0.595	0.093	0.068	-0.954	
H56944	Human arginine-rich nuclear protein mRNA, complete cds	-0.229	0.435	0.163	0.464	0.455	-0.062	
R91550	Human arginine-rich protein (ARP) gene, complete cds	-0.274	-0.002	-0.250	0.058	0.235 0.827	-0.075 -0.200	
H17975	Human armadillo repeat protein mRNA, complete cds	-0.040 -0.071	0.278 0.191	0.235 -0.772	-0.018 -0.362	-0.645	-0.200	
R01211	Human associated microfibrillar protein mRNA, complete cds	0.214	0.469	0.100	-0.010	0.260	0.194	
AA029964	Human ataxin-2 related protein mRNA, partial cds Human ATP binding cassette transporter (ABCR) mRNA, complete cds	0.131	0.335	0.119	0.335	0.197	0.104	
AA450407	Human ATPase, DNA-binding protein (HIP116) mRNA, 3' end	0.718	-0.058	0.352	0.504	0.373	0.791	
R83876	Human ATP-binding cassette protein mRNA 06B09 clone, partial cds	0.592	0.402	0.243	0.231	0.549	0.644	
AA227982	Human autoantigen DFS70 mRNA, partial cds	0.552	0.224	1.130	0.083 0.178	0.539 -0.099	0.193 -1.277	
AA481276	Human autoantigen mRNA, complete cds	0.230 -0.337	-0.448 -0.184	0.461 -0.168	-0.437	-0.099	-0.647	
AA164440	Human autoantigen pericentriol material 1 (PCM-1) mRNA, complete cds	0.324	0.428	-0.030	-0.023	0.331	-0.764	
R38717	Human autotaxin mRNA, complete cds Human B lymphocyte serine/threonine protein kinase mRNA, complete cds	0.504	0.177	-0.110	0.064	0.274	-1.467	
R50953	Human 812 protein mRNA, complete cds	0.580	0.399	0.150	0.281	0.448	0.021	
AA669637	Human B4-2 protein mRNA, complete cds	0.050	-0.111	-0.172	0.154	0.222	-0.387	
N90281	Human B7 mRNA, complete cds	-0.065	-0.063 1.166	-0.046 0.628	-0.301 0.808	-0.422 0.735	-0.075 0.187	
H52673	Human Bak mRNA, complete cds	0.732 -0.162	-0.271	-0.930	-1.026	0.462	0.496	
R43576	Human basic-leucine zipper nuclear factor (JEM-1) mRNA, complete cds Human B-cell mRNA for a member of the short-chain alcohol dehydrogenase family, partial cds	1.029	0.343	0.876	0.233	0.515	0.930	
AA113291	Human B-cell receptor associated protein (hBAP) mRNA, partial cds	0.050	0.349	0.114	0.437	-0.044	1.008	
AA460291	Human Bcl-2 binding component 6 (bbc6) mRNA, complete cds	0.579	0.991	0.801	0.683	0.396	0.841	
A A 450263	Human Rcl-2 related (Rfl-1) mRNA complete cds	-0.105	0.082	-0.176	-0.528	-0.333 0.304	-1.106 -0.786	
N48652	Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds	0.164	0.588 0.572	0.498 0.015	0.327 0.030	0.304	-0.786	
AA041400	Human beige-like protein (BGL) mRNA, partial cds	0.430 -0.071	0.071	-0.272	-0.105	0.060	-0.336	
AA778392	Human BENE mRNA, partial cds Human beta 2 gene for beta-tubulin	0.606	-0.115	0.292	0.447	0.140	-0.029	
AA043906	Human beta 2 gene for beta-tubulin Human beta 3-endonexin mRNA, long form and short form, complete cds	-0.548	-0.430	-0.565	-0.377	-0.769	0.535	
AA485653	Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds	0.393	-0.239	-0.136	0.162	0.236	0.413	
AA521339	Human beta2-chimaerin mRNA, complete cds	-0.005	-0.445	0.078	-0.587	0.400	0.542 0.467	
AA491439	Human beta2-syntrophin (SNT B2) mRNA, complete cds	0.214	0.506 0.252	-0.085 0.498	0.024 0.120	0.254 -0.217	0.674	
AA487614	Human beta-A3/A1 crystallin (CYRBA3/A1) mRNA, partial cds	0.186 0.418	0.252	0.330	0.262	0.088	0.920	
R54807	Human beta-sarcoglycan A3b mRNA, complete cds Human beta-tubulin gene (5-beta) with ten Alu family members	0.341	0.216	0.166	-0.094	0.333	0.990	
N74524 H17528	Human bHLH-PAS protein JAP3 mRNA, complete cds	0.268	0.395	-0.077	0.513	0.509	0.684	
	Human biliverdin-IXaipha reductase mRNA, complete cds	-1.111	-0.637	-1.146	-0.975	-1.006	0.222	
H39192	Human BMK1 alpha kinase mRNA, complete cds	0.444	0.296 1.128	0.122 0.754	0.229 0.855	0.347 0.856	-0.152 0.179	
R52085	Human bone morphogenetic protein-3b	0.767	1.120	0.704	5.000	0.000		

ACC	Gene Name	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
N54053	Human bone phosphoprotein spp-24 precursor mRNA, complete cds	0.806 0.739	0.619 0.923	0.182 0.118	0.253 0.619	0.688 0.569	0.529 0.451	
T98019 R44018	Human Br140 mRNA, complete cds Human brain mRNA for photolyase homolog, complete cds	0.739	0.638	0.257	0.275	0.602	-0.002	
H59916	Human brain mRNA homologous to 3'UTR of human CD24 gene, partial sequence	0.372	0.603	0.131	0.237 0.330	0.452 -0.063	0.402 0.449	
R78597	Human brain secretory protein hSec10p (HSEC10) mRNA, complete cds Human BRCA1-associated RING domain protein (BARD1) mRNA, complete cds	-0.016 0.335	-0.184 0.343	0.310 0.199	0.368	-0.191	0.466	
AA678295 N59893	Human BRCA2 region, mRNA sequence CG005	0.235	0.141	0.288	-0.037	0.674	0.870	
W80632	Human BRCA2 region, mRNA sequence CG006	0.457 0.110	0.925 0.230	0.470 0.582	0.696 0.855	0.840 0.693	0.277 0.900	
	Human BRCA2 region, mRNA sequence CG012 Human BRCA2 region, mRNA sequence CG018	0.782	0.429	-0.111	-0.535	0.601	0.885	
H29315	Human breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial cds	0.230	0.408 -0.173	0.336 0.322	0.277 0.048	0.227 -0.014	0.661 0.675	
H50323 AA449667	Human breast carcinoma fatty acid synthase mRNA, complete cds Human breast epithelial antigen BA46 mRNA, complete cds	-0.116 0.084	0.212	0.091	-0.192	0.447	0.147	
H27986	Human breast tumor autoantigen mRNA, complete sequence	-0.058	-0.075	-0.651	-0.317	-0.498	-0.016	
	Human Bruton's tyrosine kinase-associated protein-135 mRNA, complete cds	0.701 0.403	0.501 -0.035	0.433 0.241	0.120 -0.018	0.513 0.525	0.200 1.218	
H69583	Human BTG2 (BTG2) mRNA, complete cds Human BTK region clone ftp-3 mRNA	0.046	0.657	0.278	0.562	0.568	0.476	
H44785	Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds	-0.055 0.376	0.201 0.387	-0.321 0.186	-0.315 0.154	-0.162 0.642	1.074 0.710	
	Human burnetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA, complete cds Human butyrophilin (BTF1) mRNA, complete cds	0.376 0.124	0.414	0.344	0.227	0.681	0.664	
H68107 H29295	Human butyrophilin (BTF2) mRNA, complete cds	-0.255	-0.111	-0.179	0.328	-0.374	0.672 0.577	
AA478585	Human butyrophilin protein (BT3.3) mRNA, partial cds	0.160 0.140	0.500 0.510	0.292 -0.058	0.259 -0.085	0.142 -0.227	1.376	
AA253430 AA701981	Human C-1 mRNA, complete cds Human C2f mRNA, complete cds	-0.276	0.046	0.030	-0.079	0.125	0.354	
R42894	Human Ca2+-dependent activator protein for secretion mRNA, complete cds	-0.972 0.474	-0.951 0.158	0.374 0.504	-0.441 0.482	0.238 0.564	0.778 0.356	
R32410 H45976	Human Ca2+-dependent phospholipase A2 mRNA, complete cds Human cadherin-associated protein-related (cap-r) mRNA, complete cds	-0.322	-0.073	0.063	0.485	-0.077	0.651	
H51117	Human calmodulin dependent phosphodiesterase PDE1B1 mRNA, complete cds	0.378	-0.143	-0.063	-0.180 -0.018	0.095 0.303	0.364 0.662	
	Human calmodulin mRNA, complete cds	-0.076 -0.108	0.004 0.396	-0.191 0.439	0.249	0.015	0.611	
W44860 AA777637	Human calmodulin mRNA, complete cds Human calpain-like protease (htra-3) mRNA, complete cds	-0.041	0.141	0.288	0.313	0.207	0.420	
H65034	Human cAMP phoenhodiesterase mRNA 3' end	0.294	0.782 0.508	0.585 0.565	0.158 0.247	0.963 0.899	0.595 0.576	
R22790	Human cAMP responsive element binding protein beta subunit (CREBPA) mRNA, complete cds Human capping protein alpha mRNA, partial cds	0.392	0.462	0.319	-0.063	0.854	0.504	
R42609	Human capping protein alpha mRNA, partial cds	0.647	0.888 1.023	0.473 -0.335	0.028 -0.756	0.469 -0.133	0.624 0.436	
R42609	Human capping protein alpha mRNA, partial cds Human capping protein alpha subunit isoform 1 mRNA, complete cds	-0.096 0.225	0.485	0.258	0.457	0.586	0.327	
AA449753 AA099487	Human carboxylesterase (hCE-2) mRNA, complete cds	0.441	0.419	0.158	-0.011	0.547	0.128	
AA884403	Human cardiotrophin-1 (CTF1) mRNA, complete cds	-0.137 -0.181	0.168 0.435	0.010 -0.099	-0.118 0.116	0.191 0.197	0.367 0.098	
W85710	Human carnitine palmitoyltransferase I (CPTI) mRNA, complete cds Human carnitine palmitoyltransferase II precursor (CPT1) mRNA, complete cds	-0.324	-1.258	-0.443	-0.213	-0.623	-0.168	
AA418118	Human cartilage-specific homeodomain protein Cart-1 mRNA, complete cds	-0.498 0.086	-0.247 -0.001	0.012 -0.087	0.143 -0.056	0.399 -0.011	0.473 0.570	
AA052960	Human Cbf5p homolog (CBF5) mRNA, complete cds Human cbl-b mRNA, complete cds	-0.276	-0.096	-0.333	-0.028	0.179	0.621	
AA167728	Human CD27BP (Siva) mRNA, complete cds	0.184	0.480	-0.224	-0.336	1.113 0.238	-0.017 0.259	
AA410604	Human CDC16Hs mRNA, complete cds	0.844 0.114	0.950 -0.036	0.659 -0.178	0.723 -0.571	0.236	0.324	
N35067	Human cdc2-related protein kinase (CHED) mRNA, complete cds Human CDC37 homolog mRNA, complete cds	0.155	-0.103	0.523	0.853	0.081	-0.361	
N74285	Human Cdc5-related protein (PCDC5RP) mRNA, complete cds	0.064	0.074 0.377	0.258 0.375	-0.147 0.581	0.719 0.649	0.174 -0.425	
H59204	Human Cdc6-related protein (HsCDC6) mRNA, complete cds Human CDK inhibitor p19INK4d mRNA, complete cds	-0.062	0.314	0.209	-0.126	0.671	-0.033	
R77517 N72115	Human CDK6 inhibitor p18 mRNA, complete cds	0.877	1.207	0.585	0.506	0.314 0.129	0.126 0.658	
R31562	Human CDP-diacylglycerol synthase (CDS) mRNA, complete cds	0.572 -0.706	0.946 -0.084	0.406 -0.215	0.397 -0.079	0.280	0.454	
AA488332 AA676705	Human cell cycle protein p38-2G4 homolog (hG4-1) mRNA, complete cds Human cell growth regulator CGR19 mRNA, complete cds	-0.245	-0.590	-0.636	-0.847	-0.746	0.326	
N25352	Human cell surface protein HCAR mRNA, complete cds	1.810 -0.024	0.599 -0.113	1.577 -0.223	1.164 -0.089	1.808 -0.092	-0.246 -0.940	
AA436564 AA701455	Human cellular proto-oncogene (c-mer) mRNA, complete cds Human CENP-F kinetochore protein mRNA, complete cds	0.103	0.313	0.196	-0.030	-0.129	-0.185	
AA872034	Human centrin mRNA, complete cds	0.521	0.330 -0.034	0.964 0.173	1.282 0.210	1.445 0.048	0.483 -0.045	
H07880	Human chaperonin protein (Tcp20) gene complete cds Human chaperonin protein (Tcp20) gene complete cds	-0.331 0.595	0.663	0.092	-0.112	0.212	0.330	
H07880 H84982	Human checkpoint suppressor 1 mRNA, complete cds	-0.309	-0.815	-0.844	-0.595	-0.709 0.033	-0.048 0.129	
N73958	Human chemokine (TECK) mRNA, complete cds	0.072 0.122	-0.258 0.248	0.610 -0.005	-0.097 0.420	0.462	0.125	
T94579 AA402879	Human chitotriosidase precursor mRNA, complete cds Human CHL1 potential helicase (CHLR1), complete cds	-0.444	0.907	-0.473	-0.403	-0.778	0.476	
H99364	Human chloride channel protein (CLCN7) mRNA, partial cds	-0.472 -0.101	-0.343 0.240	-0.236 -0.098	-0.803 -0.002	-0.095 0.273	0.541 -0.297	
AA704459 AA426096	Human chromatin assembly factor-I p150 subunit mRNA, complete cds Human chromatin assembly factor-I p60 subunit mRNA, complete cds	0.567	0.323	0.168	0.535	1.130	-0.204	
R56871	Human chromatin assembly factor-I p60 subunit mRNA, complete cds	-0.658 0.313	-0.042 0.234	0.154 0.409	-0.619 -0.027	0.09 6 0.007	-0.133 0.760	
R56871 R21511	Human chromatin assembly factor-I p60 subunit mRNA, complete cds Human chromatin structural protein homolog (SUPT5H) mRNA, complete cds	0.224	0.475	0.350	0.284	0.832	0.694	
N47099	Human chromosome 18 Mad homolog JV18-1 mRNA, complete cds	0.322	0.392	0.315	0.240 1.520	0.261 0.193	0.216 0.314	
R83757	Human chromosome 4 Mad homolog Smad1 mRNA, complete cds Human chromosome segregation gene homolog CAS mRNA, complete cds	0.290 0.139	0.518 0.324	0.767 0.423	0.035	0.618	0.094	
N69204 W72697	Human cisolatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds	0.140	0.323	0.211	-0.251	0.377	0.111	
AA676877	Human citrate transporter protein mRNA, nuclear gene encoding mitochondrial protein, complete cds	0.678 0.150	-0.196 0.110	0.776 0.443	-0.290 -0.027	0.358 0.839	0.351 0.750	
W96155 AA873499	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1 Human class I histocompatibility antigen-like protein mRNA, complete cds	-0.282	-0.459	-0.187	-0.562	-0.287	-0.165	
AA441930	Human clathrin assembly protein lymphoid myeloid leukemia (CALM) mRNA, complete cds	0.305	0.851	0.119	0.180 0.112	-0.067 1.192	0.361 0.597	
N92864	Human cleavage and polyadenylation specificity factor mRNA, complete cds Human Clk-associated RS cyclophillin CARS-Cyp mRNA, complete cds	0.546 0.185	1.854 0.184	0.320	-0.569	0.015	0.616	
T53022	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence	0.468	1.356	-0.049	-0.101	-0.246	0.362	
R96155	Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence	0.493 -0.553	0.536 -0.277	0.291 -0.345	0.198 -0.492	-0.103 -0.314	0.494 0.467	
4 4 4004 40	Human clone 53BP1 p53-binding protein mRNA, partial cds Human clone HSH1 HMG CoA synthase mRNA, partial cds	0.364	0.410	0.028	0.295	0.017	-0.243	
AA459380) Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA, alternative	0.922	1.035 0.108	1.427 0.249	1.328 -0.002	1.324 0.044	-0.168 0.640	
AA454570	Human clone lambda 5 semaphorin mRNA, complete cds Human clone N9 Rep-8 mRNA, complete cds	0.215 -0.035	0.423	-0.630	-0.381	-0.335	0.297	
AA449440) Human clone pSK1 interferon gamma receptor accessory factor-1 (AF-1) mRNA, complete cds	-0.151	0.125	0.574	0.028 0.275	-0.285 0.564	0.445 0.842	
R40324	Human clones 23667 and 23775 zinc finger protein mRNA, complete cds Human coatomer protein (HEPCOP) mRNA, complete cds	0.680 0.013	0.515 -0.201	0.019 -0.257	-0.220	0.042	0.603	
R40212 R40212	Human coatomer protein (HEPCOP) mRNA, complete cos	0.591	0.276	-0.263	-0.754	-0.067	0.536	
AA872420	Human COL8A1 mRNA for alpha 1(VIII) collagen	0.548 0.598	-0.139 -0.019	0.632 0.166	1.199 -0.329	0.719 -0.383	0.319 0.472	
AA028903	5 Human contactin associated protein (Caspr) mRNA, complete cds 9 Human COP9 homolog (HCOP9) mRNA, complete cds	0.427	0.617	0.111	-0.019	0.526	0.616	
AA485922	Human copine I mRNA, complete cds	0.317	0.685	0.496 -0.744	0.431 -0.427	0.012 0.749	-0.018 0.163	
	Human copper transport protein HAH1 (HAH1) mRNA, complete cds Human CREB-binding protein (CBP) mRNA, complete cds	0.661 -0.064	0.990	0.024	0.061	0.021	0.546	
W89077 AA40432	7 Human CSaids binding protein (CSBP1) mRNA, complete cds	0.832	1.039	0.432	0.776	0.736	1.323 0.024	
H24301	Human CtBP interacting protein CtIP (CtIP) mRNA, complete cds	0.358 -0.270	0.538 0.110	0.291 -0.042	0.290 0.106	0.678 -0.102	0.024	
AA45400	8 Human CtBP mRNA, complete cds 4 Human CUL-2 (cul-2) mRNA, complete cds	0.445	-0.009	0.162	0.131	0.722	0.219	
R66139	Human CX3C chemokine precursor, mRNA, alternatively spliced, complete cds	0.396 0.224	0.625 0.115	0.086 -0.049	0.614 -0.158	-0.042 0.048	0.474 -0.093	
AA63008	Human cyclin-dependent kinase inhibitor p27kip1 mRNA, complete cds Human cyclin-dependent protein kinase mRNA, complete cds	0.166	0.258	0.420	0.107	0.045	0.444	
AA43050	Human cyclin-dependent protein kinase mitter, complete cds Human cyclin-selective ubiquitin carrier protein mRNA, complete cds	0.326	0.681	-0.276	-0.177	0.346	0.605	

ACC Gene Name	ZR75	YY3	YY1	468	MP1 -0.242	231 -0.275	(log base 2 ratio
AA682506 Human cyclophilin-like protein mRNA, partial cds N36882 Human c-yes-1 mRNA	0.223 0.126	0.447 0.105	-0.335 -0.110	-0.219 -0.063	0.199	-0.204	
AA011446 Human cysteine protease CPP32 isoform alpha mRNA, complete cds	-0.009	0.203	-0.153	-0.121 0.224	-0.301 0.055	0.496 0.414	
W45688 Human cysteine protease Mch2 isoform alpha (Mch2) mRNA, complete cds H68617 Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA, complete cds	0.468 0.482	0.430 0.879	-0.169 0.103	0.212	0.634	0.200	
AA873604 Human cysteine-rich heart protein (hCRHP) mRNA, complete cds	-0.619	-0.248	-0.382	-0.460	-0.208	0.291	
N59790 Human cysteine-rich sequence-specific DNA-binding protein NFX1 mRNA, complete cds	0.297 -0.196	0.533 0.771	-0.262 -0.429	-0.040 -0.509	-0.161 0.221	0.516 0.122	
R12802 Human cytochrome bc-1 complex core protein II mRNA, complete cds Human cytochrome bc-1 complex core protein II mRNA, complete cds	0.080	0.183	0.328	-0.073	0.131	-0.460	
T72604 Human cytochrome c-1 gene, complete cds	0.411 0.207	0.594 0.400	0.010 0.153	0.197 -0.282	0.285 0.172	-0.272 0.276	
T72604 Human cytochrome c-1 gene, complete cds AA495974 Human cytokine receptor (EBI3) mRNA, complete cds	0.488	1.004	0.104	-0.155	0.759	0.077	
R44290 Human cytoplasmic beta-actin gene, complete cds	0.057	0.261	-0.038 -0.304	0.122 -0.023	0.939 0.865	-0.371 -0.133	
R44290 Human cytoplasmic beta-actin gene, complete cds R60933 Human cytoplasmic chaperonin hTRiC5 mRNA, partial cds	-0.086 -0.616	0.335 -0.463	-0.414	-0.828	-0.402	0.182	
R60933 Human cytoplasmic chaperonin hTRiC5 mRNA, partial cds	0.589	-0.283	-0.437	-0.449	-0.310 0.199	0.159 0.442	
AA644679 Human cytoplasmic dynein light chain 1 (hdlc1) mRNA, complete cds	0.296 0.109	0.698 0.077	-0.103 0.373	0.126 0.235	0.359	0.429	
AA504477 Human cytoskeleton associated protein (CG22) mRNA, complete cds AA453750 Human D9 splice variant A mRNA, complete cds	0.565	0.284	-0.127	0.070	0.405	0.219	
AA129397 Human DAZ mRNA, 3'UTR	0.864 0.033	0.756 0.127	0.935 -0.369	0.147 0.066	1.172 0.059	0.257 -0.016	
AA774538 Human DAZLA mRNA, complete cds AA485944 Human DEAD-box protein p72 (P72) mRNA, complete cds	0.492	0.272	-0.142	-0.107	0.244	0.167	
R37937 Human death domain containing protein CRADD mRNA, complete cds	0.639 0.338	0.398 0.533	-0.009 -0.284	-0.013 -0.191	0.258 0.226	-0.278 -0.159	
W71984 Human death receptor 3 (DR3) mRNA, complete cds H85464 Human deleted in split hand/split foot 1 (DSS1) mRNA, complete cds	0.355	0.838	-0.103	0.015	0.612	-0.026	
AA281945 Human DENN mRNA, complete cds	-0.055	0.256 0.495	0.043 -0.238	0.020	0.696 -0.152	0.177 0.096	
AA045326 Human density enhanced phosphatase-1 mRNA, complete cds AA131238 Human dermatan sulfate proteoglycan 3 (DSPG3) mRNA, complete cds	0.088 -0.306	0.495	-0.170	-0.081	-0.267	-0.077	
AA262205 Human diacylglycerol kinase zeta mRNA, complete cds	1.013	0.781	0.333	0.687	0.457 -0.312	0.334 -0.008	
R60317 Human dihydrolipoamide dehydrogenase mRNA, complete cds	-1.647 0.166	-0.466 0.685	0.128 0.020	-1,475 -0.210	0.022	0.458	
R80317 Human dihydrolipoamide dehydrogenase mRNA, complete cds AA143437 Human DNA for rhoHP1, complete cds	0.345	0.457	-0.134	0.127	0.119	0.564	
AA487452 Human DNA fragmentation factor-45 mRNA, complete cds	-0.015 -0.554	-0.090 0.047	-0.138 -0.662	-0.279 -0.304	0.061 -0.212	0.195 0.420	
AA428377 Human DNA polymerase delta small subunit mRNA, complete cds AA402486 Human DNA repair endonuclease subunit (XPF) mRNA, complete cds	0.492	0.367	0.137	0.050	0.575	-0.463	
H20856 Human DNA repair helicase (ERCC3) mRNA, complete cds	-0.059	0.205	0.221	0.674	-0.104 0.036	-0.081 -0.087	
H20856 Human DNA repair helicase (ERCC3) mRNA, complete cds	0.723 -0.119	0.871 0.201	0.035 0.059	-0.159 0.268	0.248	0.064	
AA430675 Human DNA repair protein XRCC9 (XRCC9) mRNA, complete cds AA703660 Human DNA sequence from intron 22 of the factor VIII gene, Xq28. Contains the end of a 9.5kb repeat	0.165	0.392	0.374	-0.162	0.316	0.287 -0.127	
N21548 Human DNA topoisomerase III mRNA, complete cds	-0.348 -0.860	-0.044 0.015	-0.401 -1.141	-0.203 -0.445	-0.156 -0.854	0.184	
W88571 Human DNA-binding protein ABP/ZF mRNA, complete cds AA055885 Human DNA-binding protein CPBP (CPBP) mRNA, partial cds	0.187	0.657	0.268	0.594	0.462	0.026	
R27615 Human DNA-dependent protein kinase catalytic subunit (DNA-PKcs) mRNA, complete cos	0.018 0.102	0.398 0.240	0.135 0.391	0.410 0.629	0.208 0.280	0.525 0.390	
T73558 Human DNase1-Like III protein (DNAS1L3) mRNA, complete cds W02657 Human DOCK180 protein mRNA, complete cds	1.691	1.557	1.067	0.516	2.007	0.059	
AA465369 Human DP2 (Humdp2) mRNA, complete cds	-0.307 0.297	0.037 -0.164	-0.112 0.049	-0.123 -0.169	0.047 0.327	-0.250 -0.140	
AA406285 Human Dr1-associated corepressor (DRAP1) mRNA, complete cds AA398218 Human DR-nm23 mRNA, complete cds	-0.022	-0.025	0.191	0.389	0.617	0.267	
AA489331 Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds	0.065 0.607	0.043 0.283	0.175 0.077	-0.114 0.415	0.233 0.693	0.077 0.010	
AAA48194 Human duplicate spinal muscular atrophy mRNA, clone 5G7, partial cds AA291959 Human dynamitin mRNA, complete cds	-0.468	0.702	-0.406	-0.928	-0.519	0.610	
H09172 Human dystrobrevin-zeta mRNA, complete cds	0.435	0.499 0.549	0.384	0.318 0.160	0.803 0.616	0.278 0.416	
AA496691 Human dystroglycan (DAG1) mRNA, complete cds AA431869 Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds	0.625 -0.009	0.040	-0.145	-0.054	0.186	0.286	
AA017200 Human E2 ubiquitin conjugating enzyme Obchoc (OBChoc) mikina, complete cos	0.334	0.149	0.275	-0.188	0.162 -0.132	0.382 0.546	
R51346 Human eIF-2-associated p67 homolog mRNA, complete cds	0.505 0.395	-0.003 0.084	0.131 -0.062	-0.193 0.250	-0.132	-1.263	
R51346 Human elF-2-associated p67 homolog mRNA, complete cds AA459308 Human elastin gene, partial cds and partial 3'UTR	0.414	0.542	-0.086	0.120	0.446	-0.443	
AA629686 Human embryonic ectoderm development protein homolog (eed) mRNA, partial cds	-0.039 0.379	-0.026 0.484	-0.196 0.423	-0.266 0.922	-0.780 0.367	-0.254 0.107	
AA701655 Human endogenous retrovirus envelope region mRNA (PL1) W56771 Human endometrial bleeding associated factor mRNA, complete cds	-0.574	-0.147	1.391	-0.342	0.856	-0.111	
N66043 Human endosome-associated protein (EEA1) mRNA, complete cds	0.155 0.034	0.784 0.119	-0.083 0.342	-0.326 0.419	-0.117 0.477	0.043 -0.087	
AA680300 Human endothelial PAS domain protein 1 (EPAS1) mRNA, complete cds AA504333 Human endothelial-monocyte activating polypeptide II mRNA, complete cds	0.088	0.074	-0.283	-0.537	-0.232	-0.084	
AA127096 Human enioma gene, complete cds	-0.239 0.289	0.064 0.879	-0.180 0.215	-0.324 0.177	-0.199 0.219	0.242 0.163	
H13823 Human epidermal growth factor receptor kinase substrate (Eps8) mRNA, complete cds R71691 Human Epstein-Barr virus-induced protein mRNA, complete cds	0.412	0.362	-0.064	0.164	0.046	0.480	
AA481554 Human FRPROT 213-21 mRNA, complete cds	0.234 -0.753	0.275 -0.612	-0.074 -0.134	-0.006 0.196	0.018 -0.493	0.630 0.975	
H65734 Human erythroid-specific transcription factor EKLF mRNA, complete cds AA449459 Human estrogen sulfotransferase (STE) mRNA, complete cds	0.119	0.528	-0.051	-0.162	0.739	0.313	
AA398458 Human estrogen sulfotransferase mRNA, complete cds	0.086	0.490	0.155 0.057	0.261 0.313	0.286 0.247	0,003	
W86216 Human ets domain protein ERF mRNA, complete cds	0.152 0.487	0.283 0.515	-0.119	-0.066	0.134	-0.245	
AAA47783 Human Ets transcription factor (NERF-2) mRNA, complete cds R42479 Human ETS2 oncogene	0.206	0.343	-0.052	0.312	0.340	0.014 0.211	
R42479 Human ETS2 oncogene R54818 Human eukaryotic initiation factor 2B-epsilon mRNA, partial cds	0.641 1.920	0.896 0.950	0.425 1.429	0.280 0.850	0.634 1.450	-0.400	
R54R1R Human eukarvotic initiation factor 28-epsilon mRNA, partial cos	0.350	0.456	0.065	0.406	-0.096	0.106 0.444	
AAR76471 Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds	0.103 -0.280	0.156 -0.072	0.284 0.391	0.418 0.696	0.237 0.189	0.824	
N79484 Human extracellular matrix protein 1 (ECM1) mRNA, complete cds AA875933 Human extracellular protein (S1-5) mRNA, complete cds	0.322	-0.067	0.350	0.395	0.094	0.460	
AA262504 Human EYA3 homolog (EYA3) mRNA, complete cds	0.304 -0.261	0.467 -0.163	0.378 0.462	0.099 1.113	0.710 -0.055	0.519 0.652	
H91455 Human farnesol receptor HRR-1 (HRR-1) mRNA, complete cds AA431988 Human fatty acid amide hydrolase mRNA, complete cds	1.165	0.436	0.355	0.601	0.108	-0.211	
H79353 Human Fc-epsilon-receptor gamma-chain mRNA, complete cds	-0.263 -0.325	-0.249 -0.197	-0.077 -0.120	-0.653 -0.465	-0.136 0.229	-0.072 -0.203	
AA868113 Human FE65-like protein (hFE65L) mRNA, partial cds AA704421 Human fetal Alz-50-reactive clone 1 (FAC1) mRNA, complete cds	-0.137	0.321	-0.048	0.278	0.508	0.010	
AA020012 Human fetal brain (239FB) mRNA, from the WAGR region, complete cds	0.168 -0.100	0.286 0.198	0.551 0.068	0.787 -0.051	0.302 0.503	0.138 0.219	
AA447832 Human fetus brain mRNA for membrane glycoprotein M6, complete cds AA664077 Human fetus brain mRNA for vacuolar ATPase, complete cds	0.597	0.563	0.402	0.722	0.926	0.184	
N34095 Human FEZ2 mRNA, partial cds	-0.022	0.051	0.606	0.489 0.518	0.371 1.206	0.339 0.472	
AA405569 Human fibroblast activation protein mRNA, complete cds H19129 Human fibroblast growth factor homologous factor 1 (FHF-1) mRNA, complete cds	0.680 0.096	1.216 0.429	0.278 0.304	0.370	0.321	0.617	
N95418 Human FK-506 binding protein homologue (FKBP38) mRNA, complete cds	0.644	0.433	-0.153	-0.031 0.929	0.383 0.269	0.426 0.576	
AA630298 Human focal adhesion kinase (FAK) mRNA, complete cds	0.213 -0.073	0.395	0.173 0.481	0.006	1.337	-0.236	
AA701860 Human follistatin gene AA679177 Human follistatin-related protein precursor mRNA, complete cds	0.402	0.663	-0.131	0.294	0.237	-0.005	
N98485 Human forkhead protein FREAC-2 mRNA, partial cds	0.337 0.656	0.152 0.755	0.603 0.167	-0.057 0.237	0.193 0.333	-0.061 0.458	
AA454609 Human forkhead transcription factor HFH-4 (HFH-4) mRNA, complete cds N62761 Human fragile X mental retardation protein 1 homolog FXR1 mRNA, complete cds	0.318	0.574	0.894	1.470	0.289	0.527	
AA489628 Human fragile X mental retardation syndrome related protein (FXR2) mRNA, complete cos	0.436 0.621	0.548 0.594	0.772 0.999	2.209 2.017	0.052 0.096	0.250 0.287	
W58032 Human frezzled (fre) mRNA, complete cds N28860 Human FUSE binding protein 2 (FBP2) mRNA, partial cds	-0.025	0.149	0.020	-0.076	-0.271	0.462	
N81076 Human FUSE binding protein 3 (FBP3) mRNA, partial cds	0.614 -0.053	0.636 0.196	0.178 -0.235	0.153 -0.258	0.497 -0.058	0.232 0.590	
N75581 Human FUSE binding protein mRNA, complete cds AA421688 Human FX protein mRNA, complete cds	0.178	0.431	0.159	-0.004	0.657	0.594	
AA810225 Human G protein coupled receptor (GPCR-Br) mRNA, complete cds	-0.438	-0.209	-0.088	-0.302	-0.166	0.447	

ACC Gene Name AA450286 Human G protein gamma-10 subunit mRNA, complete cds	ZR75 -0.125	-0.404	YY1 -0.661	468 -0.767	MPI -0.174	231 0.138	(log base 2 ratio
N57964 Human G protein-coupled receptor (STRL22) mRNA, complete cds	0.287	-0.158	-0.139	-0.265 0.092	-0.123 0.443	0.312 -0.028	
H07878 Human G protein-coupled receptor GPR-NGA gene, complete cds Human G protein-coupled receptor STRL33.1 (STRL33) mRNA, complete cds	0.816 0.722	0.60B 0.840	-0.088 0.023	0.235	0.540	-0.103	
AA496947 Human G/T mismatch-specific thymine DNA glycosylase mRNA, complete cds	0.860 -0.809	1.601 -0.604	0.799 -0.587	0.310 -1.016	0.597 -0.624	-0.030 0.331	
T61948 Human G0S3 mRNA, complete cds H50677 Human g16 protein (g16) mRNA, partial cds	0.349	0.641	0.985	1.454	0.079	0.289	
H63532 Human GABA-A receptor epsilon subunit mRNA, complete cds	0.558 0.770	0.963 0.747	0.129 0.108	0.204 0.254	0.227 0.759	0.107 -0.405	
AA101225 Human GABA-A receptor pi subunit mRNA, complete cds AA868515 Human Gal beta-1,3 GalNAc alpha-2,3 sialyltransferase (ST3Gal II) mRNA, complete cds	0.220	0.229	0.476	1.291	-0.100	0.016	
AA130579 Human galectin-4 (GAL4) mRNA, complete cds	0.820 0.000	0.128 -0.293	0.572 0.859	0.186 0.182	1.687 0.176	0.288 -0.109	
AA457298 Human gammaC-crystallin (CRYGC) mRNA, complete cds H72018 Human gamma-glutamyl transpeptidase (GGT) protein mRNA, complete cds	-0.588	-0.360	0.000	0.084	0.153	-0.057	
AA129537 Human GAP SH3 binding protein mRNA, complete cds AA487426 Human GDP-dissociation inhibitor protein (Ly-GDI) mRNA, complete cds	-0.323 0.273	-0.165 0.243	-0.203 0.340	-0.296 0.587	-0.740 0.342	0.161 0.158	
AA418077 Human Gem GTPase (gem) mRNA, complete cds	-0.071	0.585	0.452 0.076	0.093 -0.496	0.389	0.253 0.427	
AA400329 Human gene for neurofilament subunit M (NF-M) AA465378 Human germline IgD chain gene, C-region, C-delta-1 domain	-0.108 0.953	-0.165 0.104	0.465	0.484	0.374	0.649	
N94385 Human germline oligomeric matrix protein (COMP) mRNA, complete cds	-0.052 0.723	0.035 0.603	0.170 -0.007	0.019 0.303	0.439 0.605	-0.535 -0.413	
AA251930 Human glioma pathogenesis-related protein (GliPR) mRNA, complete cds AA284492 Human globin gene	1.438	0.216	0.473	0.648	1.937	-0.344	
H03954 Human glucose transporter pseudogene	-0.114 -0.280	0.021 0.045	0.386 -1.144	-0.343 -0.862	-0.012 -1.169	0.183 0.066	
R44776 Human glutamate receptor (GLUR5) mRNA, complete cds Human glutamate receptor 2 (HBGR2) mRNA, complete cds	0.358	0.568	0.087	0.132	0.194 0.614	0.313 0.507	
H06193 Human glutamate receptor 2 (HBGR2) mRNA, complete cds AA428334 Human glutathione transferase Zeta 1 (GSTZ1) mRNA, complete cds	0.483 0.288	0.805 0.792	-0.103 0.369	-0.129 0.256	0.002	0.130	
AA441895 Human glutathione-S-transferase homolog mRNA, complete cds	0.165	-0.258 0.587	-0.126 0.143	-0.252 0.597	-0.104 1.559	0.145 0.218	
H16958 Human glyceraldehyde 3-phosphate dehydrogenase mRNA H16958 Human glyceraldehyde 3-phosphate dehydrogenase mRNA	0.039 0.013	0.966	-0.051	0.535	1.540	0.356	
R76808 Human glycoprotein receptor gp330 precursor, mRNA, complete cds	0.349 0.064	0.458 0.380	0.384 0.320	0.578 0.472	0.171 0.137	0.449 0.552	
AA878391 Human glypican-5 (GPC5) mRNA, complete cds AA460986 Human GPI-H mRNA, complete cds	0.243	0.128	0.203	0.456	0.497	0.149	
AA521025 Human Gps1 (GPS1) mRNA, complete cds	-0.213 -0.473	0.225 0.096	0.217 0.250	0.031 0.200	0.172 0.186	1.399 0.738	
N68193 Human Grb2-associated binder-1 mRNA, complete cds AA418008 Human growth factor independence-1 (Gfi-1) mRNA, complete cds	0.061	0.448	0.046	0.665	-0.116	0.321	
AA449678 Human GS2 mRNA, complete cds	-0.095 0.592	0.143 0.996	0.271 -0.010	0.194 0.142	0.397 0.502	0.391 0.310	
N65981 Human GT334 protein (GT334) gene mRNA, complete cds AA644191 Human GTP binding protein (ARL3) mRNA, complete cds	0.505	0.198	0.922	0.681	2.154	0.330	
AA074446 Human GTP cyclohydrolase I feedback regulatory protein gene, complete cds	-0.197 -0.200	0.001 -0.008	-0.085 -0.286	0.091 -0.404	0.079 -0.247	-0.118 1.108	
R43509 Human Gu binding protein mRNA, partial cds AA465386 Human Gu protein mRNA, partial cds	-0.016	0.589 1.249	-0.132 0.416	0.280 0.627	0.139 0.138	0.532 0.223	
H64325 Human guanine nucleotide exchange factor mRNA, complete cds R78735 Human guanine nucleotide exchange factor mRNA, complete cds	0.637 0.651	0.672	0.751	0.795	0.141	0.158	
AA012882 Human quanine nucleotide exchange factor mss4 mRNA, complete cds	1.033 0.143	0.234 0.242	2.079 0.314	0.795 0.326	1.257 0.239	0.111 0.761	
AA481277 Human guanine nucleotide exchange factor p115-RhoGEF mRNA, partial cds AA464578 Human guanine nucleotide regulatory factor (LFP40) mRNA, complete cds	0.018	-0.069	-0.647	-1.109	-0.559	0.274	
AA045822 Human quanine nucleotide regulatory protein (tim1) mkNA, complete cos	0.274 -0.226	-0.029 -0.431	0.128 -0.139	0.228 -0.871	0.320 -0.371	-0.065 -0.095	
R43581 Human guanine nucleotide-binding protein G-s, alpha subunit mRNA, partial cds R43581 Human guanine nucleotide-binding protein G-s, alpha subunit mRNA, partial cds	0.445	0.114	-0.144	-1.163	-0.018	0.398	
R43320 Human quanine nucleotide-binding regulatory protein (Go-alpha) gene	0.051 -0.252	0.028 0.164	-0.161 -0.016	0.054 -0.073	-0.245 -0.341	0.147 -1.317	
N59764 Human guanosine 5'-monophosphate synthase mRNA, complete cds AA490902 Human guanylate kinase (GUK1) mRNA, complete cds	-0.128	0.234	0.064	0.431 -0.354	0.321 -0.149	-0.116 -0.086	
AA454926 Human HBV-X associated (XAP2) mRNA, complete cds R41787 Human H-cadherin mRNA, complete cds	0.001 -0.104	-0.041 0.153	0.361	0.384	0.096	0.469	
R69885 Human HCF1 gene related mRNA sequence	-1.505 0.191	-0.453 0.238	0.008 0.166	-0.866 0.306	-0.001 0.377	-0.053 0.310	
T69012 Human heat shock protein HSPA2 gene, complete cds AA479795 Human HEM45 mRNA, complete cds	0.450	0.957	0.097	0.105	0.276	0.103	
T50313 Human hematopoietic progenitor kinase (HPK1) mRNA, complete cos	0.267 0.625	0.362 -0.095	0.323 -0.006	-0.134 0.433	0.257 0.112	0.116 0.101	
AA428321 Human heparan N-deacetylase/N-sulfotransferase-2 mRNA, complete cds AA427561 Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds	-0.058	-0.023	0.531	0.362 0.159	0.550 0.046	0.424 -0.202	
AA938757 Human heparin binding protein (HBp17) mRNA, complete cds	0.089 0.359	0.949	-0.056 1.142	1.078	1.067	-0.617	
H47076 Human hepatocyte growth factor-like protein homolog (D1F15S1A) gene, complete cas	0.717 1.854	0.622 0.713	0.059 1.581	0.510 1.480	0.643 1.827	0.318 0.106	
R72075 Human heregulin-beta1 gene, complete cds AA455303 Human hERV1 mRNA, complete cds	0.020	0.103	-0.097	0.096	-0.661	0.461	
AA132226 Human heterochromatin protein HP1Hs-gamma mRNA, complete cds	0.046 0.168	0.378 0.278	-0.046 0.159	0.003 -0.203	-0.306 0.438	0.183 0.556	
AA599176 Human heterogeneous ribonucleoprotein A0 mRNA, complete cds AA844124 Human HIG-1 mRNA, complete cds	-0.156	0.363	-0.265	0.386	0.553 0.487	0.195 0.824	
AA457697 Human high density lipoprotein binding protein (HBP) mRNA, complete cds AA191488 Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds	0.167 -0.303	0.151 -0.342	0.441 0.167	0.095 -0.364	-0.247	1.018	
H98218 Human high-mobility group phosphoprotein isoform I-C (HMGIC) mRNA, complete cas	0.529	1.140 0.118	0.048 0.345	0.105 -0.150	0.420 0.578	0.244 0.057	
AA452933 Human histone 2A-like protein (H2A/I) mRNA, complete cds AA426352 Human histone H2A.1 (H2A) gene, complete cds	0.505	0.483	0.066	0.016	0.591	-0.605	
H06295 Human histone H2B.1 mRNA, 3' end	0.361 0.257	0.437 0.471	0.441 0.330	0.269 0.232	0.343 0.550	0.152 0.045	
AA456298 Human histone H2B.1 mRNA, 3' end H06295 Human histone H2B.1 mRNA, 3' end	0.286	0.509	0.091	-0.118	0.125	0.341 1.147	
AA629558 Human histone stem-loop binding protein (SLBP) mRNA, complete cds	0.038 0.161	0.134 0.489	0.350 0.021	0.069 0.470	-0.009 0.202	-0.325	
AA425020 Human hkf-1 mRNA, complete cds AA410896 Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gen	0.853	0.731	0.790	0.554 -0.012	1.051 0.095	-0.221 0.629	
AA402960 Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gen AA454856 Human Hlark mRNA, complete cds	0.018 -1.164	0.119 -0.756	0.120 -0.295	-0.286	-0.281	0.666	
R37286 Human hnRNP core protein A1	0.091 0.773	0.378 0.666	0.087 0.198	-0.395 0.039	-0.260 0.507	0.841 0.036	
R37286 Human hnRNP core protein A1 W96058 Human hnRNP H mRNA, complete cds	-0.207	-0.121	0.107	0.129	0.030	-0.842	
W72693 Human hnRNP type A/B protein mRNA, complete cds	-0.225 0.182	-0.010 0.224	0.689 0.285	0.208 0.213	0.312 0.638	-0.432 0.195	
AA\$21026 Human hOGG1 mRNA, complete cds AA857101 Human homeo box c1 protein, mRNA, complete cds	-0.620	-0.280	-0.043	0.329	0.399	0.318	
AA447692 Human homeobox gene (clone HHO.c13)	0.440 0.450	1.005 0.306	0.041 0.594	0.795 0.101	0.324 0.669	-0.020	
AA293453 Human homeobox protein (PHOX1) mRNA, 3' end T96688 Human homeobox-containing protein mRNA, complete cds	0.200	-0.018	-0.052	0.221 -0.225	-0.259 -0.761	0.297 0.577	
H24708 Human homolog of Drosophila discs large protein, isoform 2 (hdlg-2) mRNA, complete cds A4485742 Human homolog of Drosophila enhancer of split m9/m10 mRNA, complete cds	-0.571 0.338	-0.302 0.221	-0.145 0.394	0.515	0.397	0.799	
AA702973 Human homolog of Drosophila splicing regulator suppressor-of-white-apricot mRNA, complete cas	-0.380 -0.224	-0.034 -0.117	-0.094 0.227	-0.085 0.206	0.210 -0.319	1.066 0.555	
H08820 Human homolog of yeast IPP isomerase AA504838 Human homolog of yeast mutL (hPMS1) gene, complete cds	-0.386	-0.341	-0.249	-0.287	-0.177	0.530	
A 4 80950. Human homologue of yeast sec7 mRNA complete cds	0.339 0.082	0.169 0.162	0.619 0.186	0.324 0.072	0.895 0.074	0.343 0.406	
AA456439 Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds AA424871 Human HOX4C mRNA for a homeobox protein	-0.124	0.475	0.591	0.347	0.274	0.714	
AA173290 Human HOXA1 mRNA, long transcript and alternatively spliced forms, complete cds AA626028 Human Hpast (HPAST) mRNA, complete cds	0.620 -0.141	-0.016 0.773	0.169 0.077	0.134 -0.227	0.002 0.200	1.011 0.753	
N56979 Human hPrp18 mRNA, complete cds	0.107	0.844	0.440 1.825	0.505 1.302	0.125 0.326	1.260 0.792	
AA459883 Human HRY gene, complete cds R76263 Human HS1 binding protein HAX-1 mRNA, nuclear gene encoding mitochondrial protein, complete cds	1.372 -0.076	0.178	-0.011	0.149	0.047	0.807	
AA486790 Human Hs-cul-1 mRNA, complete cds	-0.256 0.427	-0.045 1.341	0.207 -0.221	-0.642 0.336	-0.600 0.137	0.817 0.519	
N25141 Human Hs-cul-3 mRNA, partial cds AA598836 Human Hs-cul-4A mRNA, partial cds	-0.038	0.156	-0.042	-0.215	-0.186	1.021	

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ACC Gene Name	ZR75	YY3	YY1	468	MPI -0.303	231 0.584	(log base 2 r
T72030 Human hSIAH1 mRNA, complete cds	-0.263	-0.174	-0.424	-0.859 -0.519	-0.303	0.538	
AA029042 Human hSIAH2 mRNA, complete cds	0.099 2.037	0.253 0.824	-0.163 0.969	1.976	1.759	1.014	
T48741 Human Hsp27 ERE-TATA-binding protein (HET) mRNA, complete cds	-0.059	0.300	0.287	0.458	0.414	0.289	
R16849 Human HsPex13p mRNA, complete cds	-0.011	-0.084	0.617	0.237	0.076	0.371	
AA186427 Human hTRIP (hTRIP) mRNA, complete cds	-0.069	0.239	0.620	0.364	0.032	1.418	
H15747 Human HU-K4 mRNA, complete cds	-0.676	-0.593	-0.592	-0.812	-0.417	0.427	
H78385 Human huntingtin interacting protein (HIP2) mRNA, complete cds W72322 Human HuR RNA binding protein (HuR) mRNA, complete cds	0.650	0.531	0.599	0.459	0.632	-0.097	
W72322 Human HuR RNA binding protein (HuR) mRNA, complete cds AA143559 Human hVps41p (HVPS41) mRNA, complete cds	0.431	-0.003	0.150	0.349	0.423	0.053	
AA487543 Human hybrid receptor gp250 precursor mRNA, complete cds	1.450	1.464	-0.050	0.406	0.977	0.129	
AA404264 Human hypothetical protein A4 mRNA, complete cds	-0.431	-0.491	-0.844	-0.921	-0.302	-0.240	
AA702174 Human IAP homolog B (MIHB) mRNA, complete cds	-0.103	0.123	-0.272	-0.008	-0.323	0.015	
AA002126 Human IAP homolog C (MIHC) mRNA, complete cds	0.000	0.309	-0.175	0.040	-0.128	-0.165	
AA663981 Human Ig germline H-chain G-E-A region B: gamma-2 constant region, 3' end	-0.032	0.279	0.299	0.002	-0.001	0.106	
AA430668 Human IgG Fc receptor hFcRn mRNA, complete cds	-0.090	0.085	0.313	-0.002	-0.165	0.296	
AAAA2780 Human immunodeficiency virus type Lenhancer-binding protein 1	0.987	0.652	-0.152	-0.214	0.626	-0.006	
AA683219 HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2	-0.328	-0.018	0.756	-0.436	0.238	-0.697	
N63398 Human immunoglobulin-like transcript 1a mRNA, complete cds	-0.059	-0.193	-0.486	-0.056	-0.742	-0.229	
AA486221 Human inducible poly(A)-binding protein mRNA, complete cds	0.429	0.557	0.679	0.245	0.443	-0.277	
H09111 Human infant brain mRNA, clone 13cDNA73	0.387	0.364	-0.038	0.206	0.606	-0.007	
AA446018 Human Ini1 mRNA, complete cds	0.175	0.138	0.074	-0.197	0.195	0.505 0.220	
AA463931 Human inositol 1,3,4-trisphosphate 5/6-kinase mRNA, complete cds	-0.140	0.185	0.259	0.334	0.175 0.075	0.220	
H08561 Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA	-0.056	0.107	0.402	0.614 0.491	0.157	0.030	
H55921 Human insulin-stimulated protein kinase 1 (ISPK-1) mRNA, complete cds	0.240	0.161	0.242	-0.052	0.083	0.229	
AA669674 Human Int-6 mRNA, complete cds	-0.216	-0.239	0.396	0.156	0.978	-0.198	
AA443090 Human interferon regulatory factor 7 (humirf7) mRNA, complete cds	0.245	0.323	0.509 -0.417	-0.632	-0.508	-0.593	
AA490996 Human interferon-gamma induced protein (IFI 16) gene, complete cds	-0.676	-0.399 0.660	0.328	0.588	0.666	-0.414	
AA827287 Human interferon-induced leucine zipper protein (IFP35) mkNA, partial cds	0.032 -0.049	-0.257	0.053	0.507	-0.167	0.279	
AA454657 Human interleukin-11 receptor alpha chain mRNA, complete cds	1.026	0.183	0.136	0.709	0.281	-0.167	
H78244 Human intestinal and liver tetraspan membrane protein (ii-TMP) mRNA, complete cds	-0.348	-0.462	-0.935	-0.328	-0.565	0.232	
T94781 Human inward rectifier potassium channel (Kir1.3), complete cds	-0.248	0.221	-0.072	0.182	-0.109	0.759	
R43325 Human ionizing radiation resistance conferring protein mRNA, complete	-0.164	0.550	-0.774	-0.254	-0.546	0.036	
R43325 Human ionizing radiation resistance conferring protein mRNA, complete	0.096	0.299	0.026	-0.073	0.110	0.453	
AA044267 Human ionotropic ATP receptor P2X5a mRNA, complete cds	1.209	0.428	0.243	0.294	0.227	0.308	
AA133187 Human iron-regulatory protein 2 (IRP2) mRNA, partial cds R46202 Human iroquois-class homeodomain protein IRX-2a mRNA, complete cds	0.285	0.200	0.255	0.285	0.208	1.054	
AA190583 Human iroquois-class homeodomain protein IRX-2a mkNA, complete cds AL190583 Human isopeptidase T-3 (ISOT-3) mRNA, complete cds	0.200	0.506	0.240	-0.070	-0.033	-0.333	
AA419143 Human JTV-1 (JTV-1) mRNA, complete cds	0.194	0.358	0.612	0.266	0.282	-0.280	
H14383 Human K+ channel beta 2 subunit mRNA, complete cds	-0.172	0.183	-0.179	-0.364	0.048	-0.006	
AA452841 Human K-Cl cotransporter (hKCC1) mRNA, complete cds	0.555	0.223	0.083	0.336	0.168	-0.169	
AA486324 Human Ki nuclear autoantigen mRNA complete cds	0.642	0.450	-0.130	0.717	0.278	0.407	
AA146655 Human kidney mRNA for putative membrane protein with histidine rich charge clusters, complete cds	0.288	-0.010	-0.086	0.200	0.385	0.358	
AA478066 Human kinase Myt1 (Myt1) mRNA, complete cds	0.251	0.316	0.302	0.187	0.336	-0.102	
H88143 Human kinase suppressor of ras-1 (KSR1) mRNA, partial cds	0.197	0.268	0.220	-0.087	0.094	0.468	
AA504625 Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds	-0.434	-0.333	-0.529	-0.650	-0.197	0.204 0.284	
N95249 Human K-ras oncogene protein mRNA, complete cds	-0.342	-0.193	0.322	0.308	0.027 -0.078	-0.236	
N54596 Human Krueppel-related zinc finger protein (H-pik) mRNA, complete cds	-0.028	-0.414	-0.118	-0.166 0.793	0.225	0.169	
T88890 Human Krueppel-type zinc finger protein (ZNF169) gene, partial cds	1.185	1.013	0.263	-0.072	0.275	0.053	
AA455657 Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds	-0.010	0.365 -0.112	0.152 -0.299	-0.373	-0.306	0.347	
AA505045 Human L2-9 transcript of unrearranged immunoglobulin V(H)5 pseudogene	-0.244 -0.107	0.192	0.383	-0.191	0.105	0.522	
T97710 Human ladinin (LAD) mRNA, complete cds	-0.272	-0.244	0.199	0.014	0.019	0.155	
H98694 Human lambda/iota-protein kinase C-interacting protein mRNA, complete cds	0.047	0.262	0.070	0.460	-0.271	0.110	
N49751 Human LAR-interacting protein 1b mRNA, complete cds W93370 Human lectin-like type II integral membrane protein (NKG2-E) mRNA, complete cds	-0.098	-0.006	0.271	-0.024	0.391	0.026	
	0.087	-0.089	0.311	0.309	0.221	-0.016	
	0.119	0.217	0.266	-0.101	0.214	-0.083	
T55870 Human leukemia virus receptor 2 (GLVR2) mRNA, complete cos W92011 Human LGN protein mRNA, complete cds	0.729	0.184	0.343	0.105	0.817	-0.372	
AA047443 Human LIM protein (LPP) mRNA, partial cds	0.089	0.163	0.104	-0.360	-0.074	0.483	
AA195959 Human LIM protein MLP mRNA, complete cds	1.100	0.744	0.112	0.503	0.250	-0.121	
AA098980 Human lipid-activated, protein kinase PRK2 mRNA, complete cds	0.193	-0.095	0.260	0.314	-0.154	0.457	
AA017175 Human liver glutamate dehydrogenase mRNA, complete cds	0.366	-0.178	0.233	0.219	-0.321	0.549	
R54424 Human liver glutamate dehydrogenase mRNA, complete cds	0.016	0.433	-0.279	0.998	0.637 0.176	0.236 0.106	
R54424 Human liver glutamate dehydrogenase mRNA, complete cds	0.050	0.136	0.350	-0.020 0.058	0.176	0.100	
H87471 Human L-kyrurenine hydrolase mRNA, complete cds	0.007	0.207	0.293 -0.601	0.038	-0.412	0.185	
R62813 Human L-myc protein gene, complete cds	-0.205	0.343	0.560	0.391	-0.488	-0.378	
AA463204 Human LOT1 mRNA, complete cds	2.010 -0.112	-0.360	-0.449	-0.653	-0.355	0.590	
T96082 Human low-Mr GTP-binding protein (RAB31) mRNA, complete cds	0.401	0.156	0.427	0.297	0.449	0.720	
AA057378 Human low-Mr GTP-binding protein (RAB32) mRNA, partial cds	0.071	-0.129	0.297	0.083	-0.273	0.667	
R56562 Human lunatic fringe mRNA, partial cds AA867984 Human lung phospholipase A-2 (PLA-2) mRNA, complete cds, clone lung-1(hcDNA)	-0.320	-0.004	0.084	0.082	-0.285	1.072	
	0.048	0.225	0.232	-0.092	-0.482	1.118	
H99588 Human lymphoid nuclear protein (LAF-4) mRNA, complete cos AA457051 Human lymphoid-restricted membrane protein (Jaw1) mRNA, complete cds	0.585	0.572	0.521	0.245	0.755	0.202	
Hessal Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete cds	0.092	-0.065	0.407	0.250	0.033	0.353	
AA455955 Human lymphoma proprotein convertase (LPC) mRNA, complete cds	0.191	0.034	0.715	0.342	1.059	0.443	
AA458922 Human lysophosphatidic acid acyltransferase-alpha mRNA, complete cos	0.428	0.757	0.601	0.039	0.684	0.348 0.088	
T60135 Human tysophospholipase homolog (HU-K5) mRNA, complete cds	1.031	0.912	0.524	0.412	0.579		
R42153 Human lysosomal glycosylasparaginase (AGA) gene	0.072	0.250	0.040	-0.140 -0.080	0.378 0.343	-0.002 0.506	
R42153 Human ivsosomal glycosylasparaginase (AGA) gene	0.240 -0.082	0.189 0.100	-0.114 0.170	0.139	-0.065	0.473	
AA676458 Human lysyl oxidase-related protein (WS9-14) mRNA, complete cds	-0.002	0.066	-0.191	0.052	0.446	-0.569	
AA504272 Human M4 protein mRNA, complete cds	0.075	0.115	0.243	1.251	0.171	0.219	
AA485353 Human Mac-2 binding protein mRNA, complete cds	0.273	0.129	0.249	0.715	-0.060	0.738	
N62562 Human MAC30 mRNA, 3' end	0.432	-0.114	0.060	0.612	-0.311	0.711	
R23725 Human MAGE-10 antigen (MAGE10) gene, complete cds R15814 Human malate dehydrogenase (MDHA) mRNA, complete cds	-0.259	-0.391	-0.015	0.375	-0.130	0.305	
R15814 Human malate dehydrogenase (MDHA) mRNA, complete cos R15814 Human malate dehydrogenase (MDHA) mRNA, complete cos	0.051	0.465	-0.016	-0.295	-0.078	0.892	
R15814 Human malate dehydrogenase (MDHA) mRNA, complete cds A4464595 Human malignant melanoma metastasis-suppressor (KiSS-1) gene, mRNA, complete cds	0.401	0.899	0.138	0.590	0.100	0.113	
H22922 Human manic fringe precursor mRNA, complete cds	0.247	-0.206	0.181	0.078	0.052	0.074	
H07920 Human MAP kinase kinase 6 (MKK6) mRNA, complete cds	-0.048	0.664	0.016	0.322	0.132	0.650	
R39221 Human MAP kinase mRNA, complete cds	-0.171	0.131	0.027	0.237	-0.326	0.322	
AA444049 Human MAP kinase phosphatase (MKP-2) mRNA, complete cds	-0.280	0.173	-0.019	-0.379	-0.218	0.032	
W68281 Human MAPKAP kinase (3pK) mRNA, complete cds	0.142	0.160	0.440	0.147	0.388 -0.165	-0.262 0.113	
AA071473 Human matrilin-2 precursor mRNA, partial cds	-0.115	-0.192	0.101	-0.238 -1.177	-0.165	0.113	
AA029299 Human MaxiK potassium channel beta subunit mRNA, complete cds	-1.108 0.117	-0.600 0.255	-0.901 -0.113	-1.177 0.100	0.487	0.328	
T50675 Human Mch3 isoform alpha (Mch3) mRNA, complete cds	0.117	-0.051	-0.320	-0.236	-0.322	0.412	
AA281635 Human MDA-7 (mda-7) mRNA, complete cds	-0.370	-0.051	0.028	-0.230	0.079	0.876	
AA703449 Human Meis1-related protein 2 (MRG2), mRNA, partial cds	0.086	0.173	0.162	0.232	0.137	0.924	
W69649 Human MEK5 mRNA, complete cds	0.551	0.746	-0.045	-0.005	0.801	-0.149	
AA432143 Human melanocyte-specific gene 1 (msg1) mRNA, complete cds	-0.279	0.044	0.277	-0.076	0.242	0.324	
N32199 Human melanoma antigen recognized by T-cells (MART-1) mRNA AA668726 Human membrane-associated protein (HEM-1) mRNA, complete cds	0.034	-0.119	0.301	-0.409	-0.036	0.448	
	0.123	0.141	-0.014	-0.097	-0.013	0.556	
Human meningioma-expressed antigen 11 (MEA11) mixtux, partial cus R41928 Human mercurial-insensitive water channel mRNA, form 2, complete cds	0.355	0.482	0.408	-0.164	-0.300	0.214	
R41028 Human mercurial-insensitive water channel mRNA, form 2, complete cds	0.053	0.291	0.324	0.164	-0.401	0.148	
H59231 Human metalloprotease/disintegrin/cysteine-rich protein precursor (MDC9) mRNA, complete cds	0.167	-0.014	0.249	0.050	0.064	0.356	
T56281 Human metallothionein (MT)I-F gene	0.000	-0.267	0.185	-0.084	-0.158	0.330	
H72723 Human metallothionein I-B gene	0.155	0.410	-0.114	0.019	0.304	0.784	

ACC Gene Name	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
AA872383 Human metallothionein-le gene (hMT-le)	-0.331 0.795	0.094 0.535	-0.066 0.186	-0.114 -0.526	0.008	0.952 0.687	
AA292676 Human metargidin precursor mRNA, complete cds N71159 Human metastasis-associated mta1 mRNA, complete cds	0.324	0.390	-0.173	-0.040	-0.150	0.213 -0.210	
AA487589 Human methionine aminopeptidase mRNA, complete cds	1.308 -0.042	0.895 -0.110	0.503 0.328	0.024 0.193	0.120 -0.134	0.382	
AA157955 Human methyl sterol oxidase (ERG25) mRNA, complete cds N62179 Human methylmalonate semialdehyde dehydrogenase gene, complete cds	0.109	0.308	-0.500	-0.775	-0.254	-0.036	
N50834 Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds	0.252 0.234	0.522 0.124	0.268 0.411	0.418 0.384	0.203 0.328	0.290 0.281	
AA456966 Human MHC Class I region proline rich protein mRNA, complete cds AA056013 Human microfibril-associated glycoprotein-2 MAGP-2 mRNA, complete cds	-0.152	-0.234	0.472	0.232	-0.072	0.276	
H85557 Human microsomal stress 70 protein ATPase core (stch) mRNA, complete cos	0.106 0.014	0.342 -0.157	0.401 0.533	0.035 -0.262	0.298 -0.124	0.466 0.155	
H72937 Human mitochondrial 2,4-diencyl-CoA reductase mRNA, complete cds	0.645	0.469	0.287	0.108 0.070	0.328 0.404	0.160 0.315	
R53942 Human mitochondrial ADP/ADT translocator mRNA, complete cds	0.660 0.582	0.665 0.657	0.206 -0.035	0.079	0.181	-0.041	
AA173369 Human mitochondrial ATP synthase subunit 9, P3 gene copy, mRNA, nuclear gene encoding mitochon	0.697	0.133	-0.108	0.137 -0.275	0.059 0.343	0.307 0.352	
AA843592 Human mitochondrial intermediate peptidase precursor (MIPEP) mRNA, mitochondrial gene encoding AA127014 Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (MD	-0.036 0.898	-0.295 0.603	0.117 1.170	0.553	0.847	-0.266	
P31115 Human mitochondrial RNA polymerase mRNA, nuclear gene encoding mitochondrial protein, complete	0.418 0.470	0.259 0.397	0.313 0.850	0.135 0.170	0.782 0.680	0.068 0.422	
AA620477 Human mitochondrial serine hydroxymethyltransferase gene, nuclear encoded mitochondrion protein, c H37761 Human mitogen induced nuclear orphan receptor (MINOR) mRNA, complete cds	0.213	0.460	0.206	0.557	-0.010	0.223	
AA150828 Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA, complete cds	0.317 0.294	0.347 0.499	-0.207 0.308	-0.654 0.362	-0.068 -0.063	0.492 0.288	
H54888 Human mitogen-responsive phosphoprotein (DOC-2) mRNA, complete cds AA400476 Human mitotic centromere-associated kinesin mRNA, complete cds	0.145	-0.130	0.254	0.177	-0.124	0.095	
AA789301 Human modulator recognition factor I (MRF-1) mRNA, 3' end	0.710 -0.023	0.242 0.685	0.370 -0.567	0.257 -0.098	0.579 -0.846	0.145 0.041	
T64134 Human monocyte chemoattractant protein-4 precursor (MCP-4) mRNA, complete cds AA599173 Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds	0.255	0.311	-0.194	-0.029	0.528	-0.114	
AA598526 Human MOP1 mRNA, complete cds	0.032 0.284	0.435 -0.113	0.043 -0.042	0.097 -0.454	0.515 -0.314	-0.009 -0.083	
AA426312 Human Mox1 protein (MOX1) mRNA, complete cds H05820 Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3 = mammalian ribosome L3)	0.119	0.313	0.090	-0.730	0.354 0.983	0.278 0.275	
H05820 Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3 = mammalian ribosome L3)	1.091 -0.057	0.214 -0.044	1.344 0.185	0.171 0.601	0.128	0.378	
H16798 Human mRNA (HA0643) for ORF (Canis oligosaccharyltransferase 48 kDa subunit nomologue), compl	0.198	0.724	-0.096	-0.071 0.256	-0.003 0.555	0.838 0.017	
AA504128 Human mRNA export protein Rae1 (RAE1) mRNA, complete cds AA485750 Human mRNA expressed in HC/HCC livers and MoIT-4 proliferating cells, partial sequence	0.946 -0.021	0.735 0.194	0.601 0.326	0.088	-0.047	0.102	
H05893 Human mRNA for 26S proteasome subunit p97	0.515	1.271	-0.069	-0.018 0.019	0.462 0.397	0.296 0.243	
H05893 Human mRNA for 26S proteasome subunit p97	0.521 0.193	0.586 0.389	0.119 0.433	0.019	0.150	-0.440	
AA703187 Human mRNA for acetyl-coenzyme A transporter, complete cds	0.235	0.090	0.454 0.597	0.032 0.164	0.072 0.306	-0.303 0.049	
AA047478 Human mRNA for actin binding protein p57, complete cds AA862992 Human mRNA for alanine aminotransferase	0.552 -0.555	0.218 -0.236	-0.124	-0.405	-0.194	0.607	
T65118 Human mRNA for alpha-catenin, complete cds	0.400	0.231	0.060 -0.076	0.388 0.141	0.170 0.271	0.606 0.049	
T85118 Human mRNA for alpha-catenin, complete cds AA281616 Human mRNA for alpha-fetoprotein enhancer binding protein	0.248	0.356 0.398	0.185	-0.168	0.269	0.053	
AA432261 Human mRNA for ankyrin motif, complete cds	0.739 -0.646	0.325 -0.523	0.416 -0.539	0.012 -1.255	0.609 -1.206	0.501 0.332	
H19203 Human mRNA for Apo1_Human (MER5(App1-Mouse)-like protein), complete cds W80637 Human mRNA for apolipoprotein E receptor 2, complete cds	0.473	0.095	0.526	0.239	0.237	-0.284	
AA644234 Human mRNA for ATP synthase gamma-subunit (H-type), complete cds	-1.107 0.112	-1.049 0.138	-0.421 -0.228	-0.558 -0.385	0.042 0.192	-0.821 -0.031	
N27179 Human mRNA for BST-1, complete cds AA485371 Human mRNA for BST-2, complete cds	0.402	-0.071	0.394	0.126	0.751	-0.580	
AA700005 Human mRNA for CAAF1 (calcium-binding protein in amniotic fluid 1), complete cds	-0.365 0.321	-0.084 0.771	0.044	-0.646 -0.222	0.285 1.212	-0.464 -0.073	
AA464731 Human mRNA for calgizzarin, complete cds R44288 Human mRNA for calmodulin	-0.015	0.094	-0.432	-0.502	-0.181	0.182	
R44288 Human mRNA for calmodulin	0.559 0.595	0.643 0.081	0.311 0.280	0.084 -0.035	0.534 0.362	-0.125 0.245	
AA398400 Human mRNA for calponin, complete cds AA456051 Human mRNA for ceramide glucosyttransferase, complete cds	0.430	0.073	0.112	0.113	-0.030	1.886 0.123	
AA480727 Human mRNA for clathrin coat assembly protein-like, complete cds	0.945 0.978	0.479 0.762	1.107 0.124	0.489 0.418	0.746 0.766	0.068	
AA460679 Human mRNA for CMP-sialic acid transporter, complete cds	0.437	0.485	0.373 0.182	0.067 -0.410	0.460 0.268	1.306 0.516	
AA446453 Human mRNA for c-myc binding protein, complete cds R71093 Human mRNA for collagen binding protein 2, complete cds	-0.177 1.001	0.174 0.512	0.139	0.120	0.371	-0.332	
AA707922 Human mRNA for cone-specific cGMP phosphodiesterase gamma subunit, complete cds	0.512 -0.472	0.012 -0.551	-0.083 -0.150	0.027 -0.793	0.193 -0.091	-0.332 0.040	
N58511 Human mRNA for cyclin I, complete cds AA425938 Human mRNA for cysteine protease, complete cds	0.385	0.311	0.421	0.164	0.652	0.319	
R59927 Human mRNA for cytochrome c oxidase subunit VIc	0.275 0.182	-0.133 0.678	0.767 0.325	0.004 0.226	-0.319 -0.020	0.202 -0.249	
R59927 Human mRNA for cytochrome c oxidase subunit VIc T63988 Human mRNA for DB1, complete cds	1.022	0.224	0.672	0.095	0.062	-0.149	
AA487460 Human mRNA for dihydropyrimidinase related protein-2, complete cds	0.558 0.770	0.445 0.330	0.064 0.285	0.113 0.183	0.432 0.268	-0.053 -0.319	
AA707650 Human mRNA for DNA polymerase alpha-subunit	0.355	0.112	0.381	0.206 -0.506	0.170 0.822	-0.437 0.511	
AA680186 Human mRNA for EBI1-ligand chemokine, complete cds AA485427 Human mRNA for ESP1/CRP2, complete cds	-0.147 -0.012	0.018 0.279	0.119 0.702	-0.167	0.250	0.614	
H09590 Human mRNA for eukaryotic initiation factor 4AI	0.678	0.261 0.444	0.656 0.050	0.851 0.010	0.873 0.592	-0.346 0.660	
H09590 Human mRNA for eukaryotic initiation factor 4AI H05919 Human mRNA for eukaryotic initiation factor 4AII	0.210 -0.151	0.145	-0.150	-1.050	-0.578	0.502	
H05919 Human mRNA for eukaryotic initiation factor 4AII	0.873 0.240	0.805 0.397	0.231 0.317	0.223 0.455	0.286 0.134	0.217 -0.044	
N80235 Human mRNA for GC box bindig protein, complete cds AA485974 Human mRNA for golgi antigen gcp372, complete cds	0.388	0.156	0.143	-0.239	-0.165	-0.104	
AA102068 Human mRNA for heat shock transcription factor 4, complete cds	0.108 0.545	0.055 0.250	0.069 0.556	-0.238 0.128	0.052 0.460	-0.194 -0.835	
AA453749 Human mRNA for hepatoma-derived growth factor, complete cds H11069 Human mRNA for heterogeneous nuclear ribonucleoprotein D (hnRNP D)	0.078	0.248	0.356	0.529	-0.073	-0.879	
H11069 Human mRNA for heterogeneous nuclear ribonucleoprotein D (hnRNP D)	0.062 0.155	-0.048 0.243	-0.618 0.415	-0.595 0.393	-0.203 0.130	0.405 0.326	
AA180013 Human mRNA for HGF activator like protein, complete cds N98412 Human mRNA for HHR23A protein, complete cds	0.501	0.344	-0.125	0.329	0.173	0.464	
N31452 Human mRNA for histamine N-methyltransferase, complete cds	-0.249 -0.314	0.036 -0.061	-0.129 0.312	-0.025 -0.325	0.099 0.246	0.101	
R60150 Human mRNA for histidyl-tRNA synthetase (HRS)	0.336	0.296	0.393	-0.048 -0.567	0.508 -0.504	-0.049 0.472	
W81318 Human mRNA for histone H1x, complete cds	-0.490 0.255	-0.337 -0.010	-0.268 0.474	0.038	-0.161	0.342	
H05914 Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27)	0.210	0.493	0.137 0.314	0.504 0.419	1.707 1.352	-0.094 0.319	
H05914 Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) AA484566 Human mRNA for LDL-receptor related protein	0.526 0.050	0.441 -0.058	0.049	-0.117	-0.080	0.496	
AA877845 Human mRNA for LIMK-2, complete cds	0.541	0.553	-0.584 0.561	-0.516 -0.196	-0.035 -0.046	0.356 0.112	
AA176888 Human mRNA for tysosomal sialoglycoprotein, complete cds R38194 Human mRNA for LZTR-1, complete cds	0.136 -0.265	0.045	-0.323	-0.073	0.123	0.393	
H43855 Human mRNA for MDC protein	0.646 1.184	0.438 0.129	0.424 0.406	0.176 0.352	0.428 0.338	0.109 0.120	
R48926 Human mRNA for mitochobdrial enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenese alpha-subun R48926 Human mRNA for mitochobdrial enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenese alpha-subun	0.174	0.346	0.059	-0.254	-0.066	-0.460	
H23075 Human mRNA for mitochondrial 3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein, complete	-0.308 0.452	-0.288 0.539	0.165 0.363	0.307 -0.032	-0.147 0.310	-0.102 -0.272	
H23075 Human mRNA for mitochondrial 3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein, complete Human mRNA for mitochondrial 3-oxoacyl-CoA thiolase, complete cds	0.520	0.148	0.216	0.878	0.116	-0.116	
R43558 Human mRNA for mitochondrial short-chain enoyl-CoA hydratase, complet	1.974 0.163	1.137 0.339	0.593 0.275	0.749 0.041	1.264 0.153	-0.216 -0.081	
R43558 Human mRNA for mitochondrial short-chain encyl-CoA hydratase, complet AA431885 Human mRNA for MNK1, complete cds	0.161	-0.056	0.477	-0.455	0.633	0.109	
H23197 Human mRNA for MOBP (myelin-associated oligodendrocytic basic protein), complete cds, clone nOP1	-1.293 0.010	-0.750 -0.454	-1.224 -0.223	-2.096 -0.098	-1.132 -0.525	0.282	
AA857716 Human mRNA for motor protein, complete cds T46897 Human mRNA for Mr 110,000 antigen, complete cds	0.563	0.634	0.568	-0.010	0.497	0.575	

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		ZR75	YY3	YY1	468	MPI	231	(log base 2 rati
ACC	Gene Name Human mRNA for NADPH-flavin reductase, complete cds	0.764	0.874	0.116	0.752	0.480	-0.136	(log bass a lan
N76927 H45300	Human mRNA for nel-related protein 2, complete cds	0.262	0.077	0.532	-0.076	-0.096	-0.171	
N79534	Human mRNA for nel-related protein, complete cds	0.409	0.194	0.586	-0.003	0.255 0.436	-0.056 -0.667	
AA482070	Human mRNA for Neuroblastoma, complete cds	0.606 -0.438	0.361 -0.281	0.506 -0.482	0.364 -1.220	-0.313	-0.337	
AA463251	Human mRNA for nucleosome assembly protein, complete cds	0.053	0.475	0.578	0.045	0.747	0.522	
AA487588	Human mRNA for ORF, Xq terminal portion Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2	0.316	0.118	-0.185	-0.189	0.000	0.214	
W93413	Human mRNA for p52 and p64 isoforms of N-Shc, complete cds	0.317	0.222	0.531	0.242	0.091	0.071	
AA682613	Human mRNA for p97 homologous protein, partial cds	2.534	0.312	2.591	1.295	1.258	0.171	
A A 454868	Human mRNA for PDGF receptor beta-like tumor suppressor (PRLTS), complete cos	0.578	0.170 -0.639	0.613 -0.671	0.211 0.050	0.274 -0.539	0.078 -0.395	
AA007699	Human mRNA for phosphatidylinositol-glycan-class C (PIG-C), complete cds	-0.093 0.241	0.400	0.523	0.281	0.068	-0.447	
R22219	Human mRNA for phosphoethanolamine cytidylyltransferase, complete cds	0.103	0.095	0.315	0.289	-0.118	0.612	
R20554	Human mRNA for phospholipase C, complete cds Human mRNA for phospholipase C-alpha, complete cds	-0.240	0.558	-0.505	-0.220	0.336	-0.131	
R20554	Human mRNA for phospholipase C-alpha, complete cds	0.282	0.209	-0.199	0.241	-0.116	-0.102	
R44822	Human mRNA for phosphoribosypyrophosphate synthetase-associated protein 39, complete cds	0.197	-0.010	0.637 -0.435	0.430 -0.197	-0.110 -0.168	1.781 1.025	
T71686	Human mRNA for PIG-B, complete cds	0.223 -0.085	0.849 -0.412	-0.433	-0.119	0.802	0.924	
T68453	Human mRNA for PIMT isozyme I, complete cds	0.212	0.191	0.421	-0.153	-0.070	0.223	
N73625	Human mRNA for PK-120 Human mRNA for platelet activating factor acetylhydrolase IB gamma-subunit, complete cds	-0.583	0.361	0.016	-0.504	-0.488	-0.096	
R38433	Human mRNA for platelet-type phosphofructokinase, complete cds	0.179	0.083	-0.147	0.163	0.440	0.509	
R38433	Human mRNA for platelet-type phosphofructokinase, complete cds	0.356	0.361	0.210 -0.160	0.061 -0.372	0.347 -0.449	-0.257 0.010	
AA629923	Human mRNA for pM5 protein	-0.368 -0.810	-0.506 -0.374	-0.014	-0.270	-0.137	-0.554	
	Human mRNA for polyA binding protein Human mRNA for prepro cortistatin like peptide, complete cds	-0.795	-0.775	-0.405	-1.337	-0.680	0.660	
N50745	Human mRNA for pre-pro-megakaryocyte potentiating factor, complete cds	0.350	0.238	-0.083	0.028	-0.025	-0.005	
H65395	Human mRNA for proteasome activator hPA28 subunit beta, complete cds	-0.257	-0.313	-0.171	-0.130	-0.400	0.953	
AA620580	Human mRNA for proteasome subunit HsC10-II, complete cds	0.129	0.080	0.260	0.125	0.355 0.333	0.809 0.449	
N53065	Human mRNA for proteasome subunit HsC7-I, complete cds	0.245 0.418	0.095 0.128	-0.054 -0.110	0.093 -0.173	0.129	0.517	
AA403126	Human mRNA for proteasome subunit p27, complete cds	0.532	0.342	0.293	0.300	0.702	0.521	
AA424503	Human mRNA for proteasome subunit p42, complete cds Human mRNA for proteasome subunit z, complete cds	0.510	0.125	-0.049	-0.054	0.318	0.755	
AA48280	Human mRNA for protein D123, complete cds	0.121	-0.252	-0.050	-0.540	-0.146	1.045	
AA404387	Human mRNA for protein disulfide isomerase-related protein (PDIR), complete cos	0.041	-0.014	-0.171	-0.782	-0.118 2.513	1.215 0.197	
AA490473	Human mRNA for protein phosphatase 2A (beta-type)	1.610	1.325 0.090	1.458 0.084	1.509 -0.160	0.322	0.712	
AA457717	Human mRNA for proton-ATPase-like protein, complete cds	0.385 0.544	0.260	0.066	-0.122	0.160	0.040	
	Human mRNA for rab GDI alpha, complete cds	0.283	0.274	0.061	0.048	0.127	0.433	
H78788	Human mRNA for RanBP2 (Ran-binding protein 2), complete cds Human mRNA for RBP-MS/type 1, complete cds	0.640	0.102	0.405	-0.164	-0.082	0.744	
W67200 AA705069	Human mRNA for receptor of retinoic acid	-0.259	-0.247	0.497	0.030	0.434	0.831	
AA844864	Human mRNA for regenerating protein I beta, complete cds	0.067	0.161	0.442	0.513 -0.496	0.494 -0.203	0.164 0.123	
N53056	Human mRNA for renal Na+-dependent phosphate cotransporter, complete cos	-0.277 0.083	-0.116 0.294	-0.706 0.050	-0.498	0.078	0.758	
AA457719	Human mRNA for reticulocalbin, complete cds	0.620	0.391	0.324	0.240	0.446	1.350	
AA057233	Human mRNA for retinal S-antigen (48 KDa protein) Human mRNA for modanese, complete cds	-0.723	-0.542	-0.169	-0.662	-0.802	1.549	
AA465387	Human mRNA for RNA helicase (HRH1), complete cds	0.807	-0.276	0.634	-0.036	0.198	1.477	
H91647	Human mRNA for rod photoreceptor protein, complete cds	0.134	0.277	0.072	0.228 0.422	0.461 0.204	0.830 0.812	
AA465353	Human mRNA for RPD3 protein, complete cds	0.785 0.485	0.378 0.539	0.227 0.334	0.101	1.212	-0.121	
AA486403	Human mRNA for RTP, complete cds	-0.182	-0.019	0.140	-0.169	0.110	0.659	
AA425934	Human mRNA for S100 alpha protein Human mRNA for semaphorin E, complete cds	-0.349	-0.209	-0.328	-0.676	-0.256	0.966	•
H05140	Human mRNA for SMP-30 (senescence marker protein-30), complete cds	0.376	0.681	0.460	0.227	0.236	0.850	
N55480	Human mRNA for suppressor for yeast mutant, complete cds	0.237	0.235	0.252 0.287	0.117 0.027	0.568 0.535	0.907 0.614	
AA461506	Human mRNA for TESK1, complete cds	0.531 -0.631	0.816 -0.234	-0.185	-0.078	-0.396	1.108	
	Human mRNA for testis-specific TCP20, complete cds	0.413	0.494	0.476	0.587	1.238	0.666	
N52496	Human mRNA for tob family, complete cds Human mRNA for Tob, complete cds	0.805	0.286	0.650	0.097	0.380	0.392	
AAR70134	Human mRNA for TPRD, complete cds	-0.137	-0.191	0.489	-0.178	-0.171 0.956	0.700 0.762	
AA412500	Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds	0.336	0.222	0.486 -0.179	0.395 0.347	0.515	0.782	
H46554	Human mRNA for transcription factor AREB6, complete cos	-0.167 0.133	-0.157 0.349	-0.178	-0.297	-0.193	0.812	
AA450205	Human mRNA for translocation protein-1, complete cds	-1.035	-0.584	-0.468	-0.631	-1.018	0.434	
AA279188	Human mRNA for transmembrane protein, complete cds Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds	0.140	0.285	0.322	0.309	0.302	0.408	
AA479093	Human mRNA for type 2 inositol 1,4,5-trisphosphate receptor, complete cds	0.027	0.146	0.249	0.159	0.550	0.472 0.156	
AA253448	Human mRNA for U1 small nuclear RNP-specific C protein	0.513	0.693 0.558	0.327	0.173 0.001	0.357 0.026	1.178	
	Human mRNA for ubiquitin-conjugating enzyme, complete cds	1.069 0.666	0.302	0.709	0.060	0.245	0.705	
H51549	Human mRNA for UDP-galactose translocator, complete cds Human mRNA for UDP-galactose transporter related isozyme 1, complete cds	0.225	0.165	-0.021	-1.003	-0.342	0.716	
R41839	Human mRNA for uKATP-1, complete cds	0.185	0.314	-0.063	-0.309	0.371	0.748	
R20770	Human mRNA for unc-18homologue, complete cds	-0.064	0.158	0.069	0.433 -0.163	0.260 0.135	0.709 0.549	
AA69957	Human mRNA for variant hepatic nuclear factor 1 (vHNF1)	0.326 0.582	0.061 0.386	-0.027 -0.013	0.204	0.009	0.791	
AA489671	Human mRNA for XP-C repair complementing protein (p58/HHR23B), complete cds	-0.219	-0.119	-0.096	0.102	0.406	0.597	
AA66400	Human mRNA for YSK1, complete cds Human mRNA for zinc finger 5 protein, complete cds	0.274	0.055	-0.385	-1.058	-0.608	0.036	
AA03421	Human mRNA for zinc finger protein, complete cds	0.250	0.098	-0.047	0.248	-0.009	0.405 0.548	
AA40047	Human mRNA for zona-pellucida-binding protein (sp38), complete cds	0.267 0.109	0.039 0.213	0.210 -0.195	0.121 0.392	0.269 0.037	0.545	
AA42789	Human mRNA fragment encoding beta-tubulin. (from clone D-beta-1) Human mRNA, clone HH109 (screened by the monoclonal antibody of insulin receptor substrate-1 (IRS)	0.359	-0.426	-1.133	-1.123	-0.337	0.334	
AA49702	Human mRNA, clone HH109 (screened by the monocontal antibody of misdain receptor substitute in the Human msg1-related gene 1 (mrg1) mRNA, complete cds	-0.306	-0.432	-0.622	-0.776	-0.235	0.530	
AA1150/	Human msg r-telated gene i (msg r) mindox, complete cos Human mucosal addressin cell adhesion molecule-1 (MAdCAM-1) mRNA, complete cds	-0.259	-0.172	-0.171	-0.542	-0.111	0.482	
AA42989	5 Human multidrug resistance-associated protein homolog (MKP3) mKNA, partial cos	-0.146	0.079	-0.271	-0.357	-0.210	0.583 0.143	
N68159	Human multidrug resistance-associated protein homolog (MKP5) mKNA, partial cus	0.477 0.085	1.002 -0.290	0.000 -0.160	-0.038 -0.258	-0.010 0.393	0.143	
H19522	Human multiple exostosis-like protein (EXTL) mRNA, complete cds	0.874	0.814	0.095	0.682	0.013	0.813	
N24004	Human mutY homolog (hMYH) gene, complete cds 3 Human MXI1 mRNA, complete cds	-0.236	0.544	0.132	0.207	0.567	0.542	
AA/10000	5 Human myelodysplasia/myeloid leukemia factor 2 (MLF2) mRNA, complete cds	0.536	0.740	0.114	0.318	0.495	0.243	
H14359	Human myeloid eff-1 like factor (MEF) mRNA, complete cds	0.434	0.651	0.002	0.117	0.417 0.448	0.489 0.463	
H40681	Human myleoid differentiation primary response protein MyD88 mkNA, complete cos	-0.036 0.381	0.461 0.404	0.548 -0.296	0.355 0.084	0.352	0.491	
AA46134	7 Human myosin binding protein H mRNA, complete cds	0.277	0.197	-0.188	-0.220	0.196	0.583	
AA02995	6 Human myosin-IC mRNA, complete cds 3 Human myosin-IXb mRNA, complete cds	0.084	0.003	-0.135	0.093	0.034	0.111	
N66008	Human N33 mRNA, complete cds	-0.117	0.086	-0.034	-0.137	0.076	0.265	
R14692	Human Na/H antiporter (APNH1) mRNA, complete cds	1.796	0.640	1.506 0.986	0.418 0.542	2.161 1.209	0.391 0.819	
D44602	Human Na/H antinorter (APNH1) mRNA complete cds	1.711 -0.247	1.572 0.256	0.988	0.109	0.507	0.696	
	Human NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds Human NAD+dependent succinate-semialdehyde dehydrogenase (SSADH) mRNA, 3' end	-0.298	0.082	-0.186	-0.183	0.489	0.723	
H06676 T98497	Human NAD+-dependent succinate-semialdenyde denydrogenase (SSADH) hinter, 3 end Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding	0.202	-0.241	-0.188	-0.309	-0.199	0.165	
AA68032	2. Human NADH ubiquinone oxidoreductase MLRQ subunit mRNA, complete cds	0.087	-0.182	0.358	1.349	0.064	0.314	
A 4 CODE 4	5. Ulimon NADH ubiquinone ovidoreductase subunit B13 (B13) mRNA, complete cos	0.439	0.606	0.149 0.082	0.273 0.151	0.446 0.259	0.126 0.247	
AA45411	3 Human N-benzoyl-L-tyrosyl-p-amino-benzoic acid hydrolase alpha subunit (PPH alpha) mRNA, comple	0.057 0.175	0.143 0.555	0.082	0.420	0.492	0.430	
R51580	Human NECDIN related protein mRNA, complete cds Human N-ethylmaleimide-sensitive factor mRNA, partial cds	-0.279	-0.112	-0.101	-0.131	-0.012	0.124	
H97488 AA70927	Human neural cell adhesion protein (NCAM21) mRNA, complete cds	-0.354	-0.386	-0.288	-0.489	-0.471	0.730	
H29256	Human neuroendocrine/beta-cell-type calcium channel alpha-1 subunit mRNA, complete cds	0.295	-0.282	0.018	-0.326	-0.318 -0.130	0.647 1.131	
R44815	Human neuroendocrine-dig (NE-dig) mRNA, complete cds	-0.425 0.203	0.009 0.136	0.213 -0.102	0.031 0.467	0.191	1.131	
H49511	Human neurogranin (RC3) mRNA, complete cds	0.203	0.130	-0.102	5.407	5.101		

ACC	Gene Name	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
AA284329	Human neuronal membrane glycoprotein M6b mRNA, partial cds	0.024	0.764 0.270	-0.806 -0.064	-0.658 0.367	-0.646 0.247	0.678 0.480	
H26182 H22445	Human neuronal PAS2 (NPAS2) mRNA, complete cds Human neuronal pentraxin 1 (NPTX1) mRNA, complete cds	-0.523	-0.118	0.056	0.168	0.178	0.277	
H11603	Human neuron-specific vesicle coat protein and cerebellar degeneration antigen (beta-NAP) mRNA, cc Human neutral amino acid transporter B mRNA, complete cds	0.481 -0.711	1.350 -0.393	0.756 -0.738	0.752 -1.222	1.233 -0.650	0.347 0.310	
T70031 AA679278	Human NF-ATc mRNA, complete cds	-0.577	-0.934	-0.594	-0.509	-0.771	0.344 -0.147	
T72089	Human nicotinamide N-methyltransferase (NNMT) mRNA, complete cds Human nicotinamide nucleotide transhydrogenase mRNA, nuclear gene encoding mitochondrial proteir	0.599 -0.171	0.382 -0.170	0.371 -0.218	0.399 -0.075	0.500 -0.218	0.560	
H22944 T55560	Human NifU-like protein (hNifU) mRNA, partial cds	0.588	0.715	1.372	0.613	0.711 0.001	0.795 0.597	
AA625806	Human ninjurin1 mRNA, complete cds Human NK-tumor recognition molecule-related protein mRNA, complete cds	-0.210 0.320	-0.022 0.470	-0.335 -0.243	-0.437 0.210	0.321	-0.440	
W48701	Human NOF1 mRNA, complete cds	0.384	0.246	0.182	0.073	0.700	0.657 0.739	
R43217	Human non-histone chromosomal protein (NHC) mRNA, complete cds Human non-histone chromosomal protein HMG-14 mRNA, complete cds	1.405 0.286	1.673 0.984	0.923 -0.120	1.277 -0.008	-0.216	1.000	
R53889 N72057	Human non-histone chromosomal protein HMG-17 mRNA, complete cds	-0.106	0.027	0.027	-0.096 0.179	-0.011 0.548	1.229 0.350	
	Human NPAT mRNA, complete cds Human NSCL-1 mRNA sequence	0.268 -0.144	0.380 -0.139	0.045 -1.428	0.179	-1.464	-0.030	
H09936 AA485913	Human nuclear chloride ion channel protein (NCC27) mRNA, complete cds	1.184	0.627	1.027	0.588 -0.301	0.933 -0.664	-0.440 1.004	
W87528	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds Human nuclear factor NF45 mRNA, complete cds	-0.029 0.021	0.275 0.295	-0.461 0.318	0.031	0.370	0.620	
H61726	Human nuclear orphan receptor LXR-alpha mRNA, complete cds	0.278	0.466	0.443	0.749 0.127	0.315 -0.007	1.105 0.545	
T62627	Human nuclear phosphoprotein mRNA, complete cds Human nuclear protein Skip mRNA, complete cds	0.352 -0.300	1.268 0.042	-0.157 0.270	0.368	0.264	-0.096	
H17512 H05899	Human nuclear ribonucleoprotein particle (hnRNP) C protein mRNA, complete cds	0.072	0.893	0.141	0.314 -0.007	0.762 -0.016	0.599	
H05899	Human nuclear ribonucleoprotein particle (hnRNP) C protein mRNA, complete cds Human nucleolar protein p40 mRNA, complete cds	0.103 -0.523	0.570 0.094	0.706	0.203	-0.091	0.485	
R45255 AA148536	Human nucleoporin 98 (NUP98) mRNA, complete cds	-0.990	-0.413	-1.053	-0.925	-0.862 0.092	1.132 1.028	
H92201	Human nucleosome assembly protein 2 mRNA, complete cds Human nucleotide binding protein mRNA, complete cds	-0.094 -0.066	0.219 0.738	0.386	0.238 -0.044	0.101	0.648	
AA678139	Human nucleotide-binding protein mRNA, complete cds	0.337	-0.007	-0.206	-0.019 -0.706	0.465 -0.730	0.486 -0.078	
AA676802	Human OB binding protein-2 (OB-BP2) mRNA, complete cds Human occludin mRNA, complete cds	-0.823 0.099	÷0.885 0.115	-0.854 -0.142	-0.217	-0.068	0.246	
H94471 AA425655	Human Q-linked GlcNAc transferase mRNA, complete cds	0.565	0.306	0.757	0.156 -0.103	0.502 -0.031	0.920	
N62948	Human organic anion transporting polypeptide (OATP) mRNA, complete cds Human organic cation transporter 1 (hOCT1) mRNA, complete cds	0.161 0.140	0.167 2.161	-0.069 -0.316	-0.663	-0.075	0.684	
R83277	Human origin recognition complex 1 (HsORC1) mRNA, complete cds	-0.073	1.585	-0.331	-0.234	-0.441 0.166	0.164 -0.349	
N53172	Human orphan G protein-coupled receptor (RDC1) mRNA, partial cds	-0.075 0.097	0.169 0.856	0.441 -0.039	0.672 0.485	0.131	-0.345	
AA418104	Human orphan receptor mRNA, partial cds Human OS-9 precurosor mRNA, complete cds	0.080	0.063	0.550	-0.168	0.186	-0.035 0.760	
AA283693	Human osteoclast stimulating factor mRNA, complete cds	1.802 0.363	1.714 0.421	1.142 0.720	1.492 0.474	1.800 -0.022	0.726	
AA194983 W69790	Human osteoprotegerin (OPG) mRNA, complete cds Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds	0.207	1.029	-0.236	0.574	0.205	0.513 -0.297	
AAR63449	Human oviductal glycoprotein mRNA, complete cds	0.169 1.505	-0.210 1.174	-0.144 0.410	0.080 0.599	0.021 0.595	0.804	
AA034945 AA128041	Human oxidative 3 alpha hydroxysteroid dehydrogenase mRNA, complete cds Human oxidoreductase (HHCMA56) mRNA, complete cds	0.340	0.284	-0.074	0.191	0.445	0.102	
H08816	Human oxytocinase splice variant 1 mRNA, complete cds	0.342 -0.166	0.457 0.754	-0.121 -0.265	-0.146 0.379	-0.274 -0.553	0.078 0.239	
R45961	Human p105MCM mRNA, complete cds Human P13-kinase associated p85 mRNA sequence	-0.207	0.235	-0.202	0.035	-0.119	0.751	
T50139	Human p160 mRNA, complete cds	0.440 0.409	0.066 0.044	0.355 0.131	-0.058 0.118	0.354 0.149	0.906 0.863	
R94175 R70505	Human p190-B (p190-B) mRNA, complete cds Human P2U nucleotide receptor mRNA, complete cds	-0.592	-1.173	-0.947	-1.177	-0.621	1.852	
N94428	Human p300 protein mRNA, complete cds	0.281 -0.356	0.581 0.772	0.257 -0.118	0.860 0.174	0.240 0.553	0.452 0.536	
N74637 AA423870	Human p300/CBP-associated factor (P/CAF) mRNA, complete cds Human p37NB mRNA, complete cds	0.026	-0.347	-0.144	-0.178	-0.431	0.724	
AA598776	Human p55CDC mRNA, complete cds	-0.318 -0.099	-0.061 0.201	0.827 0.211	1.083 0.492	-0.019 0.203	0.829 0.741	
AA479100 AA063637	Human p76 mRNA, complete cds Human palmitoyl protein thioesterase mRNA, complete cds	-0.254	0.123	-0.119	0.221	-0.281	0.990	
W45219	Human pancreatic lipase related protein 1 (PLRP1) mRNA, complete cds Human pancreatic zymogen granule membrane protein GP-2 mRNA, complete cds	0.249 -0.237	0.313 0.176	0.606 0.166	0.471 0.463	0.709 0.062	0.022	
AA430574	Human paxillin mRNA, complete cds	0.184	0.277	0.371	0.361	0.679 -0.172	-0.120 0.210	
AA490300	Human PDGF associated protein mRNA, complete cds Human peroxisomal enoyl-CoA hydratase-like protein (HPXEL) mRNA, complete cds	-0.060 0.454	0.267 0.526	0.095 -0.112	-0.303 0.146	0.181	0.837	
AA088420	Human peroxisome proliferator activated receptor gamma 2 mRNA, complete cds	0.689	0.964	0.274	0.481 0.236	0.330 0.233	0.883 0.186	
N33331	Human peroxisome proliferator activated receptor mRNA, complete cds Human PH-20 homolog (LUCA2) mRNA, partial cds	0.006	0.496 0.405	0.223	0.521	0.592	0.243	
T64880	Human phorbolin I mRNA, partial cds	-0.458	-0.123	-0.446 0.336	-0.941 0.492	-0.837 0.165	-0.076 -0.256	
R94222	Human phosphatidylinositol (4,5) bisphosphate 5-phosphatase homolog mRNA, partial cds Human phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog mRNA, partial cds	0.399	0.718 -0.204	-0.103	-0.541	-0.145	0.320	
AA476625	Human phosphatidylinositol (4.5)bisphosphate 5-phosphatase nomolog mkna, partial cus	-0.228	-0.469 -0.222	0.129 -0.574	0.388 -0.823	-0.278 -0.469	0.753	
AA281784 H80263	Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds Human phosphatidylinositol-4-phosphate 5-kinase type II beta mRNA, complete cds	-0.309 0.509	0.787	0.335	0.551	0.289	0.312	
H57136	Human phospholemman chloride channel mRNA, complete cds	-0.248 0.261	0.445 0.612	0.211 -0.258	0.455 -0.223	0.268 0.214	-0.237 0.407	
R55490 N69672	Human phospholipase c delta 1 mRNA, complete cds Human phospholipase D mRNA, complete cds	0.221	0.583	0.175	0.306	0.237	0.189	
AA402874	Human phospholipid transfer protein mRNA, complete cds	0.387 -0.816	0.230 -0.664	0.092 -0.890	0.606 -1.277	0.237 -0.451	1.038 0.709	
AA863383	Human pim-2 protooncogene homolog pim-2h mRNA, complete cds Human PINCH protein mRNA, complete cds	0.351	1.128	1.034	-0.289	0.320	-0.060	
AA456583	Human PL6 protein (PL6) mRNA, complete cds	-0.773 0.097	-0.480 -0.406	-1.209 -0.462	-1.411 -0.158	-1.108 0.253	0.214 0.301	
H23255 AA036975	Human placenta (Diff33) mRNA, complete cds Human placenta copper monamine oxidase mRNA, complete cds	-0.070	0.258	0.603	1.050	0.140	0.594	
A A 429779	Human placenta LERK-2 (EPI G2) mRNA, complete cds	0.373 0.168	0.478 0.620	0.068	0.073 0.469	-0.038 0.259	1.023 0.385	
AA129136 H65030	Human placental equilibrative nucleoside transporter 1 (hENT1) mRNA, complete cds Human platelet-activating factor acetylhydrolase mRNA, complete cds	1.001	1.276	0.246	0.851	0.544	0.552	
AA448400	Human plectin (PLEC1) mRNA, complete cds	-0.169 0.437	0.231 -0.089	0.472	0.969 0.029	0.288 0.189	0.565 0.136	
AA459262	Human pLK mRNA, complete cds Human PMS4 mRNA (yeast mismatch repair gene PMS1 homologue), partial cds (C-terminal region)	0.360	0.237	-0.128	0.144	0.771	-0.163	
H25510	Human PMS6 mRNA (yeast mismatch repair gene PMS1 homologue), partial cos (C-terminal region)	-0.158 0.055	-0.264 0.294	-0.263 1.022	-0.580 1.538	-0.355 0.018	0.961 1.063	
AA489820	Human polyhomeotic 2 homolog (HPH2) mRNA, complete cds Human pre-B cell enhancing factor (PBEF) mRNA, complete cds	-0.399	0.232	-0.056	-0.158	0.324	0.080	
AA59881	Human preferentially expressed antigen of melanoma (PRAME) mRNA, complete cds Human preprocarboxypeptidase A2 (proCPA2) mRNA, complete cds	0.262 -0.042	0.433 0.248	1.468 0.216	2.817 0.193	0.082 -0.105	0.705	
AA42386	7 Human prepromultimerin mRNA, complete cds	-0.296	0.060	1.095	1.887	-0.170	0.533 0.459	
AA28302) Human pre-pro-orphanin FQ (OFQ) mRNA, complete cds Human pre-T/NK cell associated protein (3B3) mRNA, 3' end	-0.038 -0.027	0.366 0.215	-0.343 -0.043	0.365 0.354	0.298 -0.067	0.849	
R55188 N66396	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds	0.111	0.599	0.258	0.567	0.628	0.815 -0.406	
AA52143	Human profilin mRNA, complete cds Human prohormone convertase 5 precursor (PC5) mRNA, partial cds	-0.045 -0.073	-0.655 0.400	-0.876 0.003	-1.283 0.301	-0.571 0.237	0.731	
AA25650 R59579	Human prostaglandin D2 synthase gene	0.064	0.270	0.246	0.558	0.123	0.729 0.577	
R97308	Human prostate carcinoma tumor antigen (pcta-1) mRNA, complete cds 3 Human protease M mRNA, complete cds	0.813 -0.228	0.263 -0.335	0.787 0.147	0.757 -0.035	0.173	0.616	
AA28115	2 Human protease proMch6 (Mch6) mRNA, complete cds	1.067	0.641	0.789 -0.164	1.703	1.243 -0.730	1.193 0.986	
AA47998	Human protein A alternatively spliced form 1 (A-1) mRNA, complete cds Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds	-0.522 0.424	-0.245 0.168	0.164	1.062	0.360	0.850	
R80779	Human protein kinase (MLK-3) mRNA, complete cds	-0.123	0.183	-0.102	-0.137 2.380	0.121 0.157	1.239 1.022	
AA05367	Human protein kinase (zpk) mRNA, complete cds Human protein kinase ATR mRNA, complete cds	0.032 0.432	0.210 1.117	1.561 0.027	0.455	0.137	0.911	
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ACC	Gene Name	ZR75	YY3	YY1	468	MPI	231 1.252	(log base 2 ratio
T57556	Human protein kinase C inhibitor-I cDNA, complete cds	-0.245	0.970	-0.304	0.029 0.481	-0.432 0.489	1.305	
R37657	Human protein kinase C-binding protein RACK17 mRNA, partial cds	0.694 0.120	0.861 0.079	-0.066 1.158	1.033	0.198	0.403	
	Human protein kinase C-binding protein RACK7 mRNA, partial cds	-0.221	-0.327	0.252	-0.115	-0.069	0.750	
AA779079	Human protein kinase inhibitor p58 mRNA, complete cds	0.245	0.193	0.183	0.384	0.189	0.586	
R93912	Human protein kinase mRNA, complete cds	0.954	0.479	0.872	0.522	0.634	0.504	
	Human protein kinase PAK1 mRNA, complete cds Human protein phosphatase (KAP1) mRNA, complete cds	0.568	0.424	0.149	0.580	0.006	0.938	
AA284072	Human protein phosphatase 2A beta subunit mRNA, complete cds	0.447	0.117	0.421	0.061	0.210	1.032	
H15677	Human protein phosphatase-1 inhibitor mRNA, complete cds	0.985	-0.597	0.263	0.293	-1.157	1.427	•
AA010450	Human protein tyrosine kinase mRNA, complete cds	-0.119	0.341	-0.032	0.388	-0.037	-0.242	
AA430035	Human protein tyrosine kinase t-Ror1 (Ror1) mRNA, complete cds	-0.022	0.106	-1.133	-0.527	-0.038	0.667	
AA679180	Human protein tyrosine phosphatase 1E (PTP1E) mRNA, complete cds	0.800	1.006	0.068	0.297	0.805	0.463	
W65461	Human protein tyrosine phosphatase mRNA, complete cds	-0.233	0.046	0.310	0.178	0.246	0.563	
R79082	Human protein tyrosine phosphatase mRNA, complete cds	0.278	0.398	0.294	0.448	0.282	0.517	
R61007	Human protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds	-0.197	0.120	0.228	0.709	0.145	-0.084	
AA599145	Human protein ZW10 homolog (HZW10) mRNA, complete cds	0.695	0.291	0.386	1.262	0.115	0.871	
AA454652	Human proteinase-activated receptor-2 mRNA, complete cds	-0.610	0.182	0.688	0.045	-0.087	0.124	
AA504327	Human protein-tyrosine phosphatase (HU-PP-1) mRNA, partial sequence	0.628	0.629	0.890	0.647	-0.100	0.379	
H97140	Human protein-tyrosine phosphatase mRNA, complete cds	0.313	0.764	0.860	0.939	0.359	0.032 -0.489	
AA443558	Human protocadherin 42 mRNA, complete cds for abbreviated PC42	-0.247	-0.320	0.123	0.181	-0.102	0.079	
R89615	Human protocadherin 43 mRNA, complete cds for abbreviated PC43	0.132	-0.640	-0.369	-0.542	0.055	-0.009	
AA629603	Human PTPL1-associated RhoGAP mRNA, complete cds	0.408	0.223	0.160	0.605	0.361 0.220	-0.909	
AA664155	Human nutative 32kDa heart protein PHP32 mRNA, complete cds	-0.171	0.767 0.196	0.315 -0.122	0.432 0.052	-0.481	-0.812	
W35411	Human putative astrocytic NOVA-like RNA-binding protein (ANOVA) mkna, partial cus	-0.528 0.684	1.293	0.842	0.671	0.588	0.693	
AA700336	Human putative ATP/GTP-binding protein (HEAB) mRNA, complete cds	0.661	0.947	0.478	0.906	0.266	-0.142	
H10054	Human putative cerebral cortex transcriptional regulator 1-Brain-1 (167-1) mRNA, complete cus	0.356	0.103	0.250	0.699	0.209	0.062	
R76281	Human putative copper uptake protein (hCTR2) mRNA, complete cds	-0.316	-0.417	-0.588	-0.590	-0.550	-0.028	
H93328	Human putative cyclin G1 interacting protein mRNA, partial sequence	-0.745	-0.031	-0.782	-0.655	0.029	-1.203	
R66426	Human putative endothelin receptor type B-like protein mRNA, complete cds	0.052	0.086	0.168	0.060	0.219	0.630	
AA485665	Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds	-0.629	-0.395	-0.173	-0.351	-0.334	0.578	
AA464711	Human putative G protein-coupled receptor (AZ3B) mRNA, complete cds	1.137	0.946	0.785	1.047	-0.245	1.332	
AA521469	Human putative G-protein (GP-1) mRNA, complete cds	0.211	0.285	0.123	0.055	-0.115	1.114	
AA281549	Human putative holocytochrome c-type synthetase mRNA, complete cds	-0.264	-0.340	-0.120	-0.152	-0.403	0.266	
AA454732	Human putative IL-16 protein precursor, mRNA, complete cds	0.455	0.871	0.600	0.592	0.080	0.756	
AA454813	Human putative interferon-related protein (SM15) mRNA, partial cds	-0.423	0.213	-0.057	-0.199	0.455	0.918	
AA282936	Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds	-0.083	0.074	0.210	-0.136	0.303	0.441	
AA136566	Human putative M phase phosphoprotein 2 (MPP2) mRNA, complete cds	-0.197	0.167	0.227	0.020	0.099	0.851	
AA884935	Human putative mono-ADP-ribosyltransferase (htMART) mRNA, complete cds	-0.626	-0.124	-0.561	-0.223	-0.145	1.189	
R73608	Human putative monocarboxylate transporter (MCT) mRNA, complete cds Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds	-0.646	-0.501	-0.411	-0.361	-0.589	0.911	
AA45/118	Human putative RNA binding protein (RBP56) mRNA, complete cds	0.454	0.466	-0.223	-0.208	0.050	0.216	
AA85/343	Human putative RNA binding protein (RDF36) filters, complete cds	-0.035	0.153	0.173	0.465	0.034	0.913	
AAU54287	Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds	-0.091	0.087	0.380	-0.012	-0.179	1.087	
	Human putative splice factor transformer2-beta mRNA, complete cds	-0.695	-0.349	-0.284	-0.142	-0.084	0.511	
H11720 R56149	Human putative transmembrane protein (nma) mRNA, complete cds	0.279	0.237	-0.225	0.846	-0.370	0.287	
A A A R 2 A R D	Human putative transmembrane receptor IL-1Rrp mRNA, complete cds	0.444	-0.150	1.115	0.578	0.144	0.723	
W96450	Human putative tRNA synthetase-like protein mRNA, complete cds	-0.165	-0.108	-0.281	0.148	-0.713	0.647	
W73892	Human putative tumor suppressor (LUCA15) mRNA, complete cds	-0.414	-0.457	0.047	-0.137	0.310	0.002	
H65676	Human putative tumor suppressor (SNC6) mRNA, complete cds	-1.193	-0.342	-0.586	-0.721	-0.269	0.008	
H52729	Human PWP2H protein mRNA, complete cds	-0.211	-0.198	-0.266	-0.023	-0.412	1.145	
AA158035	Human pyridoxal kinase mRNA, complete cds	-0.180	-0.063	0.076	0.272	0.332	1.084	
H11346	Human pyrroline-5-carboxylate dehydrogenase (P5CDh) mRNA, long form, complete cds	0.044	-0.083	0.528	0.314	-0.060	0.971 0.639	
R23735	Human R kappa B mRNA, complete cds	-0.200	-0.137	0.902	-0.073	0.132		
H82236	Human RACH1 (RACH1) mRNA, complete cds	0.708	-0.146	0.108	0.543	0.154 0.042	0.815 -0.263	
W84445	Human Rad mRNA, complete cds	0.327	0.155	0.063	0.455	-0.591	0.587	
H99196	Human Rad50 (Rad50) mRNA, complete cds	-0.294	-0.212	-0.602	-0.279 0.338	0.177	0.769	
H19201	Human Rai guanine nucleotide dissociation stimulator mRNA, partial cds	0.329	0.624	-0.069	0.365	0.237	1.051	
AA401972	Human RalGDS-like 2 (RGL2) mRNA, partial cds	0.216	0.305	0.118 0.259	0.223	0.331	0.807	
W32474	Human rap2 mRNA for ras-related protein	0.482 0.513	0.508	0.041	0.341	0.149	1.495	
T60070	Human Rar protein mRNA, complete cds	0.303	0.223	0.177	0.307	0.547	0.855	
R83224	Human ras inhibitor mRNA, 3' end	0.324	-0.048	0.070	0.473	0.371	1.068	
	Human ras inhibitor mRNA, 3' end	-0.181	-0.235	-0.283	-0.663	-0.425	0.993	
W32272	Human RasGAP-related protein (IQGAP2) mRNA, complete cds	0.269	-0.236	0.070	0.174	0.439	1.115	
AA626787	Human ras-related C3 botulinum toxin substrate (rac) mRNA, complete cds	-0.006	0.179	0.090	0.728	0.233	0.666	
	Human ras-related small GTP binding protein Rab5 (rab5) mRNA, complete cds	0.207	0.538	0.024	0.324	0.489	0.276	
N70362	Human RecA-like protein (hREC2) mRNA, complete cds	0.223	0.190	-0.579	-0.518	0.556	0.921	
R53998	Human recepin mRNA, complete cds Human receptor 4-1BB ligand mRNA, complete cds	0.488	0.367	0.250	0.148	0.590	0.570	
AA778003	Human receptor protein tyrosine phosphatase hPTP-J precursor, mRNA, complete cds	-0.092	0.140	-0.148	0.004	-0.124	0.762	
	Human reelin (RELN) mRNA, complete cds	-0.038	-0.297	-0.231	-0.398	0.022	0.997	
R45102	Human regulator of G-protein signaling similarity (RGS7) mRNA, partial cds	0.429	0.316	0.113	1.199	-0.117	0.268	
H24326	Human renal cell carcinoma antigen RAGE-1 mRNA, complete putative cds	-0.380	-0.140	-0.256	-0.281	0.427	0.704	
N62873	Human requiem (HREQ) mRNA, complete cds	0.742	1.346	-0.099	0.024	0.083	0.683	
AA458807	Human retinal protein (HRG4) mRNA, complete cds	0.083	0.014	0.115	-0.198	-0.075	0.381	
N98563	Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds	-0.046	0.856	-0.364	-0.537	-0.089	1.172	
AA865464		0.589	0.182	-0.374	-0.393	0.162	1.162	
W96099	Human retinoid X receptor-gamma mRNA, complete cds	-0.435	0.318	-0.574	-0.342	-0.556	0.578 -0.206	
AA007419	Human RGP4 mRNA, complete cds	0.419	0.268	0.635 0.078	0.720 0.696	0.361 0.546	0.404	
T57805	Human Rho-associated, coiled-coil containing protein kinase p160ROCK mRNA, complete cds	-0.027	0.576	0.128	0.005	0.396	-0.115	
AA701545	Human ribonuclease k6 precursor gene, complete cds	-0.070 0.089	0.372 -0.146	0.990	0.925	-0.372	-0.005	
AA434088	Human ribosomal protein L10 mRNA, complete cds	0.009	0.065	0.182	0.331	0.312	0.864	
	Human ribosomal protein L35 mRNA, complete cds	0.487	-0.390	0.389	0.337	-0.024	0.716	
W84472	Human ribosomal protein S6 mRNA, complete cds	0.196	-0.296	-0.214	-0.314	0.146	0.822	
AA42594	Human RIG mRNA, complete sequence	-0.009	-0.154	-0.080	-0.175	-0.117	1.548	
AA085618	Human RLIP76 protein mRNA, complete cds	0.328	0.359	0.239	0.047	0.456	-0.187	
AAU4/25	Human RNA binding protein Etr-3 mRNA, complete cds Human RNA polymerase II elongation factor ELL2, complete cds	-0.542	-0.295	-0.306	-0.295	-0.418	0.807	
AA19124	Human RNA polymerase if elongation ractor Ecc2, complete costs Human RNA polymerase II holoenzyme component SRB7 (SRB7) mRNA, complete cds	-0.333	-0.002	0.273	-0.040	-0.036	1.023	
AA13003	Human DNA actumente il subunit (hsRPR10) mRNA, complete cos	-0.592	-0.308	-0.003	-0.552	-0.587	1.226	
H15431	Human RNA polymerase II subunit hsRPB4 mRNA, complete cds, and ribosomal protein S26 pseudog	1.148	-0.579	1.357	0.135	1.424	0.468	
AA477421	Human RNA polymerase II subunit hsRPB7 mRNA, complete cds	0.179	0.006	0.828	-0.317	0.295	0.681	
AADROOR	Human RNA polymerase Itl subunit (RPC62) mRNA, complete cds	0.413	0.228	0.103	-0.193	0.428	1.202	
R15111	Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, complete cds	-0.565	-0.160	0.042	-0.061	-0.461	1.233	
AA45895	Human RNaseP protein p30 (RPP30) mRNA, complete cds	0.258	0.269	0.098	0.192	0.107	1.425	
AA19503	Human Ro/SSA ribonucleoprotein homolog (RoRet) mRNA, complete cds	-0.035	-0.183	-0.146	-0.079	-0.263	0.509	
	Human RP3 mRNA, complete cds	-0.234	-0.092	-0.039	0.094	-0.296	1,215	
AA23533	Human RSU-1/RSP-1 mRNA, complete cds	0.198	0.377	0.111	0.221	-0.094	1.252	
AA45610	Human scaffold protein Pho1 mRNA, complete cds	-0.240	0.356	-0.071	-0.092	0.399 -0.086	0.805 2.177	
AA67725	Human scavenger receptor cysteine rich Sp alpha mRNA, complete cds	0.127	-0.133	-0.010	-0.197 0.136	-0.079	2.177	
AA70816	Human scr3 mRNA for RNA binding protein SCR3, complete cas	-0.150	0.390	-0.096 0.101	0.136	0.174	0.128	
AA46495	7 Human Sec7p-like protein mRNA, partial cds	-0.227	-0.093 0.752	0.101	0.342	0.660	-0.010	
AA66913	8 Human SEF2-1A protein (SEF2-1A) mRNA, 5' end	0.547 0.358	0.752	0.695	0.510	0.800	-0.090	
AA48808	1 Human selenium donor protein (selD) mRNA, complete cos	-0.540	-0.255	-0.283	-0.399	-0.695	0.281	
T65736	Human setenium-binding protein (hSBP) mRNA, complete cds	-0.227	-0.209	-0.107	0.225	-0.606	0.939	
	9 Human selenoprotein W (selW) mRNA, complete cds	-0.525	0.291	-0.020	-0.167	0.190	1.317	
N50444	Human semaphorin (CD100) mRNA, complete cds	3.023						

ACC Gene Name	ZR75	YY3	YY1	468	MPI	-0.026	(log base 2 ratio
AA455145 Human semaphorin V mRNA, complete cds	-0.416 0.721	0.280 -0.040	-0.152 0.468	-0.081 0.397	0.241 1.957	-0.026	
AA630604 Human serine kinase mRNA, complete cds AA427740 Human serine/threonine kinase mRNA, partial cds	0.113	0.568	-0.065	0.465	0.153	-0.309	
N54551 Human serine-threonine phosphatase (PP5) mRNA, partial cds	0.978 0.076	0.619 0.095	0.248 -0.216	0.002 -0.190	1.014 -0.355	0.619 0.923	
AA757429 Human serotonin N-acetyltransferase mRNA, complete cds N35241 Human ser-thr protein kinase PK428 mRNA, complete cds	0.043	0.397	0.083	0.119	0.156	1.226	
AA496795 Human SH3 domain-containing protein SH3P17 mRNA, complete cds	0.828	1.139	0.470 0.551	-0.118 0.222	0.526 0.513	1.221 0.479	
N94713 Human SH3 domain-containing protein SH3P18 mRNA, complete cds AA398366 Human SH3-containing protein EEN mRNA, complete cds	0.161 -0.262	0.075 0.275	-0.455	0.189	-0.200	0.841	
AA458661 Human short-chain alcohol dehydrogenase (XH98G2) mRNA, complete cds	-0.186	0.220	0.000	-0.129	0.286	0.176 0.607	
AA630094 Human sigh binding protein 1 (SighBP1) mRNA, partial cds	0.472 0.774	0.669 0.595	0.011 -0.146	0.860 0.783	0.264 0.794	0.804	
H19111 Human sialytransferase (STX) mRNA, complete cds AA497051 Human sialytransferase SThM (sthm) mRNA, complete cds	0.035	0.051	0.000	0.075	0.134	1.090	
W47485 Human sigma receptor mRNA, complete cds	0.018 0.302	0.055 0.137	-0.008 0.340	-0.255 0.234	0.019 0.394	1.120 0.486	
AA488622 Human signal transducing adaptor molecule STAM mRNA, complete cds AA504624 Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds	-0.458	0.127	-0.367	-0.330	-0.299	0.370	
AAASROCK Human signaling lymphocytic activation molecule (SLAM) mKNA, complete cos	1.162	0.473	0.338	0.577 0.458	0.745 0.819	0.824 0.703	
N68166 Human signal-transducing quanine nucleotide-binding regulatory (G) protein beta subunit mRNA, comp. Human SLP-76 associated protein mRNA, complete cds	0.093	0.063 0.396	-0.167	0.232	0.647	0.313	
AA496780 Human small GTP binding protein Rab7 mRNA, complete cds	0.696	0.577	0.743	0.481	0.629	0.739	
H98534 Human small GTP binding protein Rab9 mRNA, complete cds	0.604 0.351	0.702 0.165	-0.072 0.141	0.482 0.140	0.774 0.697	1.012 0.683	
AA399674 Human small proline rich protein (sprll) mRNA, clone 1292 H16824 Human Smg GDS-associated protein SMAP mRNA, complete cds	-0.628	-0.182	-0.353	-0.310	0.208	0.980	
AA457731 Human SNARE protein Ykt6 (YKT6) mRNA, complete cds	0.248 0.165	0.406 0.417	0.400 0.393	1.118 -0.104	0.275 -0.057	0.949 0.613	
AA489246 Human SNC19 mRNA sequence AA487575 Human Snk interacting protein 2-28 mRNA, complete cds	0.647	1.154	0.388	0.561	0.554	1.077	
T62520 Human SnRNP core protein Sm D2 mRNA, complete cds	-0.162	0.953	-0.355	-0.277	-0.334	0.694 0.818	
H60423 Human sodium phosphate transporter (NPT3) mRNA, complete cds	0.380 -0.499	0.171 -0.506	0.165 -0.944	0.238 -0.727	0.411 -0.267	0.936	
AA858296 Human sodium phosphate transporter (NPT4) mRNA, complete cds R51912 Human somatostatin I gene and flanks	-0.050	-0.193	0.177	-0.076	-0.729	-0.708	
AA699361 Human spliceosomal protein (SAP 49) gene, complete cds	-0.140 0.943	0.207 0.651	-1.058 1.021	-0.896 1.971	-0.016 1.326	0.410 0.742	
AA633757 Human spliceosome associated protein (SAP 145) mRNA, complete cds Human splicesomal protein (SAP 61) mRNA, complete cds	0.037	0.109	0.008	-0.132	0.173	0.526	
AA491213 Human splicing factor SRp30c mRNA, complete cds	0.083	0.196	0.245	0.155 0.420	0.289 -0.297	0.769 0.923	
AA598965 Human splicing factor SRp40-1 (SRp40) mRNA, complete cds	-0.110 -0.003	0.160 0.034	0.185 0.357	0.013	-0.014	0.083	
AA169645 Human splicing factor SRp55-2 (SRp55) mRNA, complete cds AA182847 Human SPS1/STE20 homolog KHS1 mRNA, complete cds	0.027	0.488	0.091	0.045	0.476	0.169	
H53703 Human squamous cell carcinama of esophagus mRNA for GRB-7 SH2 domain protein, complete cos	-0.521 -0.191	-0.071 -0.195	-0.010 0.378	-0.476 -0.004	-0.282 -0.195	0.149 0.251	
AA485141 Human Src-like adapter protein mRNA, complete cds AA425823 Human SREBP-1 mRNA, complete cds	-0.062	0.133	0.198	0.246	-0.227	0.751	
AA464529 Human Ste20-like kinase (MST2) mRNA, complete cds	-0.243	0.117 0.090	-0.096 0.092	-0.033 -0.183	0.347 -0.071	0.866 -0.116	
H05935 Human sterol 27-hydroxylase (CYP27) mRNA, complete cds H05935 Human sterol 27-hydroxylase (CYP27) mRNA, complete cds	0.410 0.738	0.897	0.072	0.090	0.325	-0.079	
AA701914 Human sterol regulatory element binding protein-2 mRNA, complete cds	-1.135	0.052	-0.160	-1.380	-1.002	-0.145 0.023	
AA598637 Human stimulator of TAR RNA binding (SRB) mRNA, complete cds	0.331 0.223	0.355 0.282	0.085 -0.153	0.087 0.139	0.560 0.297	0.586	
T95014 Human stress responsive serine/threonine protein kinase Krs-2 mRNA, complete cds AA045500 Human stromelysin-3 mRNA	0.453	0.485	0.453	0.661	0.005	0.681	
R40897 Human succinyl CoA:3-oxoacid CoA transferase precursor (OXCT) mRNA, complete cds	0.587	0.599	0.249 -0.003	0.233 -0.034	0.610 0.528	0.022 -0.082	
AA463642 Human sulfite oxidase mRNA, complete cds	0.418 -0.170	0.464 0.144	0.071	0.548	-0.169	-0.916	
W88655 Human sulfotransferase mRNA, complete cds R52548 Human superoxide dismutase (SOD-1) mRNA, complete cds	-0.004	-0.318	-0.071	-0.409	-0.048	-0.296	
R5254R Human superoxide dismutase (SOD-1) mRNA, complete cos	0.014 0.643	-0.183 0.585	-0.079 -0.154	-0.287 0.351	-0.222 0.237	-0.055 0.484	
AA485355 Human suppressor of cytokine signalling-1 (SOCS-1) mRNA, complete cds R73545 Human surface antigen mRNA, complete cds	0.474	0.232	0.243	0.362	0.863	0.223	
AA449715 Human sushi-repeat-containing protein precursor (SRPX) mRNA, complete cds	-0.425	0.028	0.312	0.719 -0.561	0.071 -0.287	-0.032 -0.459	
AA872122 Human SWI/SNF complex 155 KDa subunit (BAF155) MRNA, complete cds	-0.807 -0.493	-0.509 -0.993	-0.461 -1.256	-1.305	-0.679	0.082	
Hosest Human SWI/SNF complex 60 KDa subunit (BAF60a) mRNA, alternatively spliced, complete cos	0.252	0.255	0.360	0.132	0.134	-0.337	
AA478436 Human SWI/SNF complex 60 KDa subunit (BAF60b) mRNA, complete cds	-0.445 -0.355	-0.024 -0.075	0.767 -0.012	0.768 -0.108	0.533 -0.084	0.144 0.686	
AA053810 Human SWI/SNF complex 60 KDa subunit (BAF60c) mRNA, complete cds W74377 Human symplekin mRNA, complete cds	0.631	0.632	0.372	0.146	0.388	0.763	
AA488635 Human synaptobrevin-3 mRNA, complete cds	0.167 0.213	0.255 1.649	0.319 -0.279	0.750 0.073	0.313 -0.157	0.608 -0.078	
H15539 Human syntaxin 1A mRNA, complete cds AA436871 Human syntaxin 3 mRNA, complete cds	-0.144	-0.025	0.158	0.521	0.115	-0.467	
T71551 Human syntaxin 7 mRNA, complete cds	0.467	0.608 -0.002	0.270 -0.169	0.127 -0.152	0.773 0.661	-0.287 0.063	
AA732931 Human syntaxin mRNA, complete cds R37743 Human T54 protein (T54) mRNA, complete cds	-0.355 0.069	-0.002	-0.254	0.083	0.365	-0.021	
W8884 Human TAR DNA-binding protein-43 mRNA, complete cds	-0.439	-0.624	-0.743	-1.424	-0.777	-0.134 -0.741	
AA436409 Human TAR RNA binding protein (TRBP) mRNA, complete cds	0.627 1.064	0.004 0.367	0.089 1.115	1.020 0.449	0.824 0.578	-0.848	
N62244 Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds H94949 Human tastin mRNA, complete cds	0.275	0.403	0.121	0.215	0.301	-0.444	
AA017043 Human tat interactive protein mRNA, complete cds	0.448 -0.141	0.440 -0.164	0.262 -0.235	0.234 -0.272	0.425 -0.113	-0.115 -0.464	
AA235706 Human TATA-binding protein associated factor 30 kDa subunit (tafil30) mRNA, complete cds AA857131 Human Tat-SF1 mRNA, complete cds	-0.340	0.049	0.120	0.341	0.315	0.189	
AA598483 Human tax1-binding protein TXBP151 mRNA, complete cds	0.266 -0.090	0.135 -0.094	0.434 0.071	0.042 0.604	0.460 -0.388	-0.927 -1.033	
AA718910 Human tax1-binding protein TXBP181 mRNA, complete cds AA482067 Human tazarotene-induced gene 2 (TIG2) mRNA, complete cds	0.258	0.268	0.137	0.034	0.255	-0.323	
H11501 Human TB1 gene mRNA, 3' end	0.492	0.813	0.229	0.381	0.508 0.704	0.121 -0.661	
AA487148 Human TBP-associated factor (hTAFII130) mRNA, partial cds	0.858 -0.188	1.017 0.977	0.251 -0.336	0.537 0.262	-0.042	-0.322	
H11783 Human TBP-associated factor TAFII80 mRNA, complete cds R87763 Human telencephalin precursor mRNA, complete cds	-0.339	0.295	0.182	-0.044	0.184	0.908	
AASAARAA Human terminal transferase mRNA, complete cds	1.766 -0.561	0.275 -0.473	1.268 -0.123	1.181 -0.325	1.956 -0.024	0.008 -0.361	
AA291773 Human tetracycline transporter-like protein mRNA, complete cds AA291718 Human tetratricopeptide repeat protein (tpr1) mRNA, complete cds	0.280	0.032	0.605	0.325	0.483	0.074	
H09811 Human tetratricopeptide repeat protein (tpr2) mRNA, complete cos	0.442	0.326	0.131	0.010	0.274 0.541	-0.210 -0.745	
T55801 Human TFIIA gamma subunit mRNA, complete cds	0.778 0.185	0.852 0.357	0.236 -0.267	0.430 0.216	-0.125	1.152	
AA453787 Human TFIIB related factor hBRF (HBRF) mRNA, complete cds AA063580 Human TFIID subunit TAFII55 (TAFII55) mRNA, complete cds	-0.280	0.564	0.101	0.156	0.970	0.234	
AA045588 Human TFIID subunits TAF20 and TAF15 mRNA, complete cds	-0.194 0.027	0.411 0.319	0.081 0.278	-0.027 0.373	0.805 0.508	-0.298 0.420	
AA843718 Human TFillC Box B-binding subunit mRNA, complete cds AA481279 Human Tg737 mRNA, complete cds	0.764	0.931	0.211	0.438	0.446	0.509	
R79935 Human TGF-beta inducible early protein (TIEG) mRNA, complete cds	-0.186	-0.230	-0.033	-0.532 0.157	-0.296 0.192	-0.441 0.281	
AA029497 Human thymidine kinase 2 (TK2) mRNA, complete cds	0.290 0.798	-0.070 0.389	0.355 0.276	0.157 0.082	0.192	0.933	
AA634103 Human thymosin beta-4 mRNA, complete cds R01238 Human tip associating protein (TAP) mRNA, complete cds	0.119	0.575	0.223	-0.009	0.376	0.039	
AA456295 Human TNF receptor associated factor 6 (TRAF6) mRNA, complete cds	-0.245 -0.699	0.192 -0.144	0.330 -0.648	0.235 -0.670	0.708 -0.275	0.389 0.650	
H54629 Human TNF-related apoptosis inducing ligand TRAIL mRNA, complete cds T57791 Human Toll-like receptor 2 (TLR2) mRNA, complete cds	0.281	0.060	0.416	0.339	0.141	0.153	
R76099 Human Toll-like receptor 3 (TLR3) mRNA, complete cds	-0.530	0.270	-0.184 -0.016	-0.415 0.949	0.295 0.200	-0.054 -0.006	
N41021 Human Toll-like receptor 5 (TLR5) mRNA, partial cds	0.600 1.046	-0.179 0.176	-0.009	-0.220	1.128	0.124	
R60160 Human topoisomerase I mRNA, complete cds	0.179	0.458	0.212	-0.025	0.178	0.054 1.018	
AA134814 Human TRAF-interacting protein I-TRAF mRNA, complete cds	0.365 0.593	0.283	0.369 0.235	-0.018 -0.542	0.202 -0.541	0.102	
AA035144 Human transcription factor (MEF2) mRNA, complete cds AA394236 Human transcription factor ERF-1 mRNA, complete cds	0.332	0.477	0.273	0.183	0.549	0.061	
AA496359 Human transcription factor ETR101 mRNA, complete cds	0.387	0.325	0.266	0.563	0.475	-0.117	

		ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
ACC Gene Name H77652 Human transc	ription factor hGATA-6 mRNA, complete cds	0.371	0.584	-0.025	0.239	0.943	0.457	(log base 2 raise
T72202 Human transc	ription factor IL-4 Stat mRNA, complete cds	0.477	0.578	0.186	0.350	0.332 0.137	0.362 0.390	
AA488618 Human transc	ription factor LSF mRNA, complete cds	0.074 -0.121	0.148 -0.021	0.120 0.087	-0.211 -0.382	0.340	0.251	
AA490903 Human transc	ription factor mRNA, complete cds ription factor NFATx mRNA, complete cds	0.353	0.450	0.082	0.003	0.547	-0.469	
W74602 Human transc	ription factor RTEF-1 (RTEF1) mRNA, complete cds	0.156 -0.074	0.342 0.221	-0.203 -0.304	0.223 0.127	0.103 0.187	-0.582 0.379	
AA069372 Human transc	ription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds ription initiation factor TFIID subunit TAFII31 mRNA, complete cds	-0.089	0.157	0.056	-0.197	0.300	0.418	
H05655 Human transc	riptional activator mRNA, complete cds	0.210	0.085	-0.026	-0.284	0.303	0.599	
AA099534 Human transc	riptional coactivator PC4 mRNA, complete cds	-0.484 -0.615	0.101 -0.115	-0.490 -0.472	-0.317 -0.317	-0.701 -0.348	0.123 -0.831	
H89996 Human transc	riptional regulator hornolog RPD3 mRNA, complete cds riptional repressor (CTCF) mRNA, complete cds	0.334	0.291	0.142	0.030	0.662	-0.398	
AA488645 Human transc	riptional repressor (NAB1) NAB1 mRNA, complete cds	-0.122	0.268	0.470	0.118 -1.406	-0.031 -0.364	-0.362 0.275	
AA496630 Human transc	ucin-like enhancer protein (TLE3) mRNA, complete cds	-1.068 0.629	-0.970 0.416	-1.103 0.140	0.105	0.673	0.741	
	ucin-like protein mRNA, complete cds ormer-2 alpha (htra-2 alpha) mRNA, complete cds	0.436	0.327	0.007	-0.010	0.426	-0.514	
AA779457 Human transf	orming growth factor-beta (tgf-beta) mRNA, complete cds	0.142	0.358	0.148	0.343 -1.137	0.533 -0.398	0.154 0.360	
AA156324 Human transg	lutaminase mRNA, 3' untranslated region	-0.723 0.532	-1.258 0.488	-0.607 0.289	0.077	0.663	-1.005	
W60015 Human transl	tion initiation factor eIF-2alpha mRNA, 3'UTR tion initiation factor eIF-3 p110 subunit gene, complete cds	0.024	0.165	0.379	0.566	-0.051	-0.103	
R54097 Human transl	itional initiation factor 2 beta subunit (elF-2-beta) mRNA, complete cds	0.355	0.363	0.375	0.187 0.013	0.356 0.347	0.143 0.047	
R54097 Human transl	ational initiation factor 2 beta subunit (elF-2-beta) mRNA, complete cds	0.299 -0.210	0.480 0.458	0.185 0.015	0.103	0.377	1.178	
R93621 Human transl R45413 Human transr	ational initiation factor 2 beta subunit (elF-2-beta) mRNA, complete cds nembrane 4 superfamily protein (SAS) mRNA, complete cds	0.138	-0.245	0.226	-0.329	-0.223	0.733	
N94921 Human transf	nembrane receptor (ror2) mRNA, complete cds	-0.025	0.366	-0.199 0.271	0.334 0.775	0.691 0.382	0.626 0.254	
AA481067 Human transp	ortin (TRN) mRNA, complete cds	0.350 1.529	0.171 0.584	0.835	0.696	1.855	0.786	
AA496800 Human transp AA404293 Human triadir	mRNA complete cris	0.238	0.228	0.421	0.099	0.400	0.254	
T65861 Human tRNA	guanine transglycosylase mRNA, complete cds	1.295	0.733	0.615	0.563 0.031	0.718 0.323	0.274 0.961	
AA598982 Human trophi	nin mRNA, complete cds	0.173 0.014	0.279 0.478	0.104 -0.053	0.031	0.323	0.874	
T72398 Human trypto	phan oxygenase (TDO) mRNA, complete cds 2 protein mRNA, complete cds	0.411	0.263	0.312	0.201	0.462	0.462	
AA884015 Human tubby	related protein 2 (TULP2) mRNA, complete cds	-0.196	0.055	D.268	0.068	0.004 0.513	0.253 -0.305	
AA504618 Human tubuli	h-folding cofactor E mRNA, complete cds	0.443 0.578	0.109 0.271	0.204 0.299	0.424 0.444	0.120	-0.604	
AA497020 Human tumoi T55353 Human tumoi	necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds necrosis factor type 2 receptor associated protein (TRAP3) mRNA, complete cds	0.927	0.222	0.493	0.526	0.179	0.129	
AA670215 Human tumoi	susceptiblity protein (TSG101) mRNA, complete cds	0.277	0.015	0.461	-0.121	0.236 0.596	1.044 0.784	
N62620 Human two P	domain K+ channel TWIK-1 mRNA, complete cos	0.474 0.405	0.218 0.252	-0.298 0.433	0.082 0.156	0.503	0.375	
T51849 Human tyrosi	ne kinase (HTK) mRNA, complete cds I-tRNA synthetase mRNA, complete cds	0.645	0.124	0.682	0.338	0.556	-1.394	
R36571 Human U1 sr	RNP-specific protein A gene	-0.219	-0.356	-0.019	0.139 -0.244	-0.416 -0.693	-0.431 -0.726	
R36571 Human U1 sr	RNP-specific protein A gene	0.258 -0.321	-0.409 -0.049	-0.139 -0.225	-0.244	0.192	1.393	
T67521 Human U2AF	1-RS2 mRNA, complete cds tin carrier protein (E2-EPF) mRNA, complete cds	0.484	0.501	-0.008	0.168	0.244	1.250	
T57841 Human ubiqu	tin fusion-degradation protein (UFD1L) mRNA, complete cds	1.640	0.410	0.080	0.033	0.826 0.478	0.910 0.326	
AA454143 Human ubiqu	tin protease (Unph) proto-oncogene mRNA, complete cds	0.153 0.322	-0.131 0.957	0.262	0.163	0.520	-0.848	
R61332 Human ubiqu R61332 Human ubiqu	tin-activating enzyme E1 (UBE1) mRNA, complete cds tin-activating enzyme E1 (UBE1) mRNA, complete cds	0.234	0.621	0.367	0.196	0.115	-0.389	
AA488626 Human ubiqu	tin-homology domain protein PIC1 mRNA, complete cds	0.848	-0.127	0.492 0.502	0.313 0.355	0.210 0.603	1.403 1.192	
	e diphosphoglucose pyrophosphorylase mRNA, complete cds	0.788 0.455	0.303 0.227	0.302	0.165	0.477	1.381	
T82469 Human uropo T82469 Human uropo	rphyrinogen III synthase mRNA, complete cds rphyrinogen III synthase mRNA, complete cds	0.247	0.238	-0.079	-0.267	-0.086	0.913	
AARREA33 Human vacuu	lar protein sorting homolog h-vps45 mRNA, complete cds	-0.118	-0.205 0.521	-0.052 -0.123	0.452 0.250	-0.541 0.235	0.755 0.282	
H07899 Human vascu	lar endothelial growth factor related protein VRP mRNA, complete cos	0.578 0.373	-0.196	0.595	-0.559	0.198	0.570	
AA666180 Human v-erb	oinding protein-1 (VBP-1) mRNA, partial cds	0.478	0.403	0.366	-0.051	0.813	0.777	
AA460728 Human voltage	e dependent anion channel form 3 mRNA, complete cas	0.824 -0.466	0.150 -0.244	-0.023 -0.310	0.176 -0.691	0.347 -0.260	0.814 0.560	
R36947 Human volta	e-gated calcium channel beta subunit mRNA, complete cds	0.213	-0.447	-0.450	-0.185	0.143	0.903	
AA449975 Human WS-3	epeat protein HAN11 mRNA, complete cds mRNA, complete cds	1.585	2.163	1.960	1.693	2.679	0.530 1.105	
W31391 Human X104	mRNA, complete cds	-0.090 0.123	0.207 0.189	-0.173 0.071	0.172 -0.185	-0.046 0.519	0.277	
R55789 Human X11	rotein mRNA, partial cds x repressor mRNA, complete cds	0.413	0.499	0.045	0.513	0.295	0.046	
T64885 Human X2 b AA425395 Human X-lini	ed PEST-containing transporter (XPCT) mRNA, partial cds	0.591	0.466	0.079	-0.084	0.139	-0.506 0.065	
T00724 Human VMD	mPNA complete cds	0.210 0.160	0.062 0.252	0.266 0.283	0.151 0.407	0.923 0.211	0.352	
R49530 Human Xq28 R49530 Human Xq28	cosmid, creatine transporter (SLC6A8) gene, complete cds, and CDM gene, partial cds cosmid, creatine transporter (SLC6A8) gene, complete cds, and CDM gene, partial cds	0.431	0.591	-0.352	-0.058	0.176	0.242	
AA443950 Human YL-1	mRNA for YL-1 protein (nuclear protein with DNA-binding ability), complete cds	2.138	0.334	0.639	0.727	2.035	0.340 0.318	
W73810 Human YMP	mRNA, complete cds	-0.304 1.489	-0.263 0.578	-0.800 0.409	-0.500 0.568	-0.008 1.121	-0.227	
AA758082 Human YY1-	associated factor 2 (YAF2) mRNA, complete cds inger protein (MAZ) mRNA	-0.388	-0.509	-0.591	-0.511	-0.082	0.030	
AA001276 Human zinc	inger protein (SRF-ZRP) mRNA, 3' end	-0.501	-1.201	-0.875	-1.176	-0.577	0.156 0.037	
W79396 Human zinc	inger protein C2H2-25 mRNA, complete cds	0.567 1.081	0.559 0.080	0.467 0.195	0.272 -0.249	0.399 0.413	-0.116	
T47230 Human zinc	inger protein mRNA, complete cds inger protein mRNA, complete cds	0.003	-0.159	0.113	-0.319	-0.364	0.395	
AA418251 Human zinc	inger protein PLAG1 mRNA, complete cas	0.655	0.147	0.007 -0.622	0.283 -0.095	-0.049 0.323	0.439 0.747	
W73060 Human zinc	inger protein RIZ mRNA, complete cds	-0.012 0.132	-0.233 0.443	0.015	0.660	0.149	0.139	
H22826 Human zinc-	inger domain-containing protein mRNA, partial cds inger protein C2H2-150 mRNA, complete cds	0.107	-0.027	-0.697	-0.613	-0.509	-0.467	
AA055504 Human zinc-	inger protein mRNA, complete cds	0.378	0.594	-0.170	0.108 -0.370	-0.020 0.406	0.351 0.563	
R58985 Human Zn-1	5 related zinc finger protein (rif) mRNA, complete cds	0.302 0.599	0.166	-0.133 -0.007	0.036	0.421	0.500	
H20759 Human zygir	I mRNA, complete cds related protein ZRP-1 mRNA, complete cds	0.670	0.756	0.095	0.063	0.482	0.797	
N93941 HUMMLC2A	; Homo sapiens; ; 593 base-pairs	0.571	0.284	0.547 0.165	0.151 0.080	0.115 0.751	1.027 1.902	
AA454612 Huntingtin (H	untington disease)	0.433 0.080	0.396 0.426	0.165	1.060	-0.403	1.126	
A 6 0 4 0 2 2 2 Mudro vou acut	nediated motility receptor (RHAMM) Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydrat	ε 0.211	-0.050	0.174	-0.136	0.644	0.501	
AA411202 Hydroxyacyl	Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A nydrati	į 0.369	0.397 0.292	-0.119 -0.032	0.162 0.474	0.713 0.111	0.558 0.936	
R68803 Hydroxy-deft	a-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	0.178 0.576	0.590	0.173	0.007	0.223	0.759	
AA495858 Hydroxymett W95082 Hydroxysten	yibitane synthase iid (11-beta) dehydrogenase 2	0.173	0.169	0.213	-0.076	0.989	0.958	
AA437291 Hydroxysten	id (17-beta) dehydrogenase 3	0.575 -0.710	0.307 -0.449	0.551 0.001	0.445 0.118	0.466	0.410 0.231	
N47312 Hypoxanthin	e phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	-0.710	-0.449	-0.183	-0.143	0.073	0.505	
AA873762 HZF-16 N62482 I factor (com	plement)	0.784	0.589	0.335	0.796	0.485	0.862	
H44953 ICH-2 PROT	EASE PRECURSOR	0.519 0.215	0.525 0.379	0.359 0.013	0.335 0.180	0.313 0.500	1.064 0.704	
	sulfatase (Hunter syndrome)	-0.445	0.627	-0.750	-0.650	0.228	0.403	
AA457705 IEX-1 H28469 IG ALPHA-2	CHAIN C REGION	0.570	0.530	-0.067	-0.133	0.362	0.343 0.299	
R39227 IK		0.305 0.033	0.618 -0.267	0.060 -0.378	0.154 -0.797	0.760 -0.564	0.759	
	-EARLY RESPONSE PROTEIN NOT ulin gamma 3 (Gm marker)	0.423	0.084	0.059	-0.012	-0.283	1.030	
	OBULIN J CHAIN	0.276	0.012	0.206	-0.051 0.590	0.236 0.526	-0.537 -0.248	
	ulin lambda light chain	0.785 0.627	0.470 0.757	0.829 0.150	0.106	0.184	0.473	
H73590 Immunoglob T86934 Immunoglob	ulin mu ulin-associated alpha	1.149	0.547	0.881	0.630	0.526	0.379	
. J J								

	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
ACC Gene Name R72079 Immunoglobulin-associated beta (B29)	0.126	0.301	0.227	0.034	0.865	0.526	(-2
W73790 IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR	0.510 -0.411	0.542 0.013	0.195 0.052	1.179 -0.230	0.195 0.189	0.851 -0.778	
R52542 IMP (inosine monophosphate) dehydrogenase 1 AA478279 Indole 2,3-dioxygenase	-0.342	0.087	-0.189	-0.152	-0.025	-0.302	
N27159 Inhibin, beta A (activin A, activin AB alpha polypeptide)	0.011 -0.104	-0.093 -0.207	0.593 -0.389	0.593 0.123	0.098 0.112	-0.546 0.221	
H82442 Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein AA482119 Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	0.218	0.024	-0.071	-0.126	0.695	0.323	
AA464856 Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	0.471 -0.121	0.650 0.484	0.009 0.152	-0.036 -0.007	0.113 0.486	0.581 0.831	
H18070 INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR AA701976 Inositol 1,4,5-triphosphate receptor, type 3	0.376	0.271	-0.048	-0.255	0.434	-0.089	
R94153 Inositol 1,4,5-trisphosphate 3-kinase B	0.000 0.706	0.251 1.189	0.087 0.176	0.412 0.103	0.087 0.599	0.328 0.264	
AA279072 Inositol polyphosphate phosphatase-like protein 1 (51C protein) H52141 Inositol polyphosphate-1-phosphatase	-0.145	-0.120	0.254	0.132	0.186	0.156	
AA001614 Insulin receptor	-0.006 0.096	0.658 0.082	0.256 0.463	-0.005 -0.170	-0.147 0.199	0.444	
AA456704 Insulin receptor substrate-1 [human, skeletal muscle, mRNA, 5828 nt] W86199 INSULIN-DEGRADING ENZYME	1.481	0.816	1.193	1.484	0.413	0.784	
R16073 Insulin-like 4 (placenta)	0.092 0.110	0.146 -0.092	0.179 0.087	0.491 0.324	-0.024 -0.059	0.543 0.521	
AA456321 Insulin-like growth factor 1 (somatomedia C) AA256419 Insulin-like growth factor 1 receptor	0.958	0.613	0.384	0.476	0.807	0.382	
N74623 Insulin-like growth factor 2 (somatomedin A)	0.495 0.563	0.247 1.113	0.134 0.419	0.088 0.471	0.556 0.934	0.543 0.374	
T62547 Insulin-like growth factor 2 receptor AA233185 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR	-0.072	0.281	0.538	0.406	0.143 -0.299	0.620 0.722	
H79047 Insulin-like growth factor binding protein 2 (36kD) AA598601 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR	0.267 0.165	-0.027 0.566	0.416 0.090	0.279 0.145	0.362	0.608	
T52830 Insulin-like growth factor binding protein 5	0.452	0.317	-0.074	-0.137	0.565 0.613	0.607 0.517	
AA478724 Insulin-like growth factor binding protein 6	0.312	0.100 0.377	0.248 0.247	0.022 -0.210	0.885	0.499	
R38640 Insulinoma-associated 1 (symbol provisional) AA419177 INTEGRAL MEMBRANE PROTEIN E18	0.249	0.197	-0.416	0.150 -0.258	-0.303 -0.112	0.929 0.462	
R68805 Integral transmembrane protein 1	-0.326 0.641	-0.061 0.658	-0.065 0.049	0.062	0.743	0.405	
AA424695 Integrin alpha-3 subunit AA485668 Integrin beta-4 subunit	-0.257	-0.166	0.293	0.418 0.064	-0.415 -0.482	-0.725 0.067	
AA434397 Integrin beta-5 subunit	-0.377 -0.365	-0.469 -0.242	0.034 0.126	0.396	-0.482	0.050	
AA463257 Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) H79341 Integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	-0.398	-0.059	-0.615	-0.646	0.104 -0.009	-1.103 0.227	
R43483 Integrin, alpha 6	-0.558 1.934	0.470 1.739	-0.059 1.054	-0.449 0.761	1.663	0.540	•
AA055979 Integrin, alpha 78 AA425451 Integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	0.426	0.962	0.292	0.537	0.493	-0.212 -0.354	
R48766 Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) AA436187 Integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophac	-0.270 0.029	-0.183 0.188	0.125 -0.144	0.581 -0.253	-0.144 0.220	0.781	
AA029934 Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	0.173	0.270	0.024	-0.110	0.542 1.225	0.084 0.121	
N64384 Integrin, alpha X (antigen CD11C (p150), alpha polypeptide)	1.234 -0.568	0.499 -0.417	1.027 -0.033	1.135 0.174	-0.251	-0.312	
W68403 Integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1	-0.591	-0.475	-0.030	0.195 -0.162	-0.434 -0.034	0.707 0.270	
AA666269 Integrin, beta 3 (platelet glycoprotein Illa, antigen CD61)	0.210 0.344	-0.321 0.537	0.499 0.309	0.337	0.187	0.621	
AA037229 Integrin, beta 3 (platelet glycoprotein Illa, antigen CD61) W56754 Integrin, beta 8	1.317	-0.128	0.287	1.066 0.301	1.155 0.001	0.720 -0.006	
R06580 INTER-ALPHA-TRYPSIN INHIBITOR COMPLEX COMPONENT II PRECURSOR	-0.095 0.440	0.118 0.202	0.548 0.269	0.095	0.817	-0.083	
R77293 Intercellular adhesion molecule 1 (CD54), human minovirus receptor R21535 Intercellular adhesion molecule 2	1.077	0.558	0.231	1.140	0.888	0.277	
AA479188 Intercellular adhesion molecule 3	0.249 0.139	0.204 0.104	0.451 0.267	0.509 0.237	0.138	0.277	
AA485426 Interferon (alpha, beta and omega) receptor 2 AA878880 Interferon (gamma)-induced cell line; protein 10 from	-0.125	0.143	0.815	-0.269	0.221 1.467	0.177 0.533	
T47815 INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR	2.149 0.696	0.497 0.825	1.067 -0.115	0.456 0.258	0.326	0.328	
AA478043 Interferon regulatory factor 1 AA416883 Interferon regulatory factor 2	0.772	0.546	0.393	0.270 0.290	0.500 -0.041	0.770 -0.234	
AA825491 Interferon regulatory factor 4 N30372 Interferon regulatory factor 5	-0.067 0.290	-0.281 0.187	0.100 -0.255	-0.017	-0.100	0.031	
AA157813 INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN	0.284	0.540 0.568	-0.815 0.253	0.280 0.434	-0.008 1.147	0.497 0.271	
N59150 INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR H11482 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR	0.389 -0.221	-0.057	0.512	0.414	0.283	0.295	
AA406020 INTERFERON-INDUCED 17 KD PROTEIN	-0.013 0.196	0.334 0.422	-0.108 0.063	-0.037 -0.119	0.169 0.415	0.358 0.511	
N63988 INTERFERON-INDUCED 54 KD PROTEIN W72748 INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 2	0.147	0.240	0.325	0.369	0.491	0.032	
AA489640 Interferon-inducible 56-KDa protein	0.559	0.472 -0.138	0.290	0.464 -0.380	0.359 -0.302	0.438 -0.008	
AA862371 INTERFERON-INDUCIBLE PROTEIN 1-8D AA464417 INTERFERON-INDUCIBLE PROTEIN 1-8U	0.184	-0.164	0.101	0.134	0.499	-0.072	
AA419251 INTERFERON-INDUCIBLE PROTEIN 9-27	0.453 -0.002	0.510 0.197	0.405 0.203	0.016 0.497	0.548 0.172	0.227 0.545	
T72877 Interleukin 1 receptor antagonist AA936768 Interleukin 1, alpha	0.462	0.737	0.487	0.183	0.548	0.402	
AA150507 Interleukin 1, beta	1.622 -0.073	1.661 -0.576	0.361 -0.263	-0.289 -0.525	1.937 -0.394	1.310 0.390	
AA437226 Interleukin 10 receptor N59270 Interleukin 15	-0.743	0.530	-0.679	-1.169	0.051	0.163	
AA054754 Interleukin 15 receptor alpha chain AA057204 Interleukin 2 receptor beta chain	-0.194 -0.307	0.211 -0.045	0.129 -0.009	0.680 0.445	0.045 -0.305	0.441	
N54821 Interleukin 2 receptor gamma chain	0.722	0.450 -0.467	0.539 -0.658	0.360 -0.369	0.413 -1.524	0.332 0.498	
AA293306 Interleukin 4 receptor N98591 Interleukin 6 (B cell stimulatory factor 2)	-0.531 0.635	0.638	0.155	0.115	0.528	0.185	
AA485865 Interleukin 7 receptor	0.761 0.903	0.773 1.010	0.256 -0.119	0.366 0.494	0.661 1.041	0.150 0.016	
AA102526 Interleukin 8 R56553 INTERLEUKIN ENHANCER-BINDING FACTOR	-0.231	-0.120	0.439	0.428	0.097	0.024	
T95052 INTERLEUKIN-1 BETA CONVERTASE PRECURSOR	-0.056 -0.428	-0.054 -0.176	-0.007 0.014	0.244 0.343	-0.214 0.013	0.925 0.501	
AA454526 INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR H78386 INTERLEUKIN-1 RECEPTOR, TYPE II PRECURSOR	-0.426	0.109	0.658	1.291	-0.125	0.102	
AA464528 INTESTINAL MEMBRANE A4 PROTEIN	-0.006 0.471	0.150 0.559	0.834 0.507	1.170 0.283	-0.093 0.574	0.579 0.355	
N74131 INTESTINAL TREFOIL FACTOR PRECURSOR AA156988 Iron-responsive element binding protein 1	0.613	0.351	-0.348	0.113	-0.274	-0.440	
AA018683 ISL1 transcription factor, LIM/homeodomain, (islet-1)	0.485 -0.161	0.237 0.285	0.854 -0.373	0.167 -0.173	1.526 -0.236	-0.460 -1.222	
AA679907 Isocitrate dehydrogenase 2 (NADP+), mitochondrial AA410636 Isoleucine-tRNA synthetase	1.068	0.813	0.367	-0.186	0.697	0.320	
AA464149 Isovalery! Coenzyme A dehydrogenase	1.070 0.553	0.993 0.385	0.476 0.451	0.405 0.418	0.376 0.042	0.347 0.519	
AA284634 Janus kinase 1 (a protein tyrosine kinase) AA293365 JNK ACTIVATING KINASE 1	1.281	0.602	1.295	0.476	1.193	0.443	
N94468 Jun B proto-oncogene	-0.027 0.734	-0.137 0.816	-0.217 0.478	0.433 0.285	0.181 0.517	0.873 0.334	
AA131585 Jun D proto-oncogene H17883 Kalimann syndrome 1 sequence	0.592	0.790	0.379	0.068	0.403	-0.388 -0.652	
AA011415 Kell blood group precursor (McLeod phenotype) AA479882 Keratin 10 (epidermotytic hyperkeratosis; keratosis palmaris et plantaris)	0.054 -0.063	0.488	-0.096 0.114	0.120 0.541	0.007	-0.089	
W60057 Keratin 13	0.073	0.039	-0.203	-0.251 0.393	0.342 1.352	0.346 0.474	
AA664179 Keratin 18	1.057 0.429	1.516 -0.263	0.008 0.148	0.019	0.370	0.497	
AA629189 Keratin 4 AA160507 Keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)	0.315	2.322 -0.396	0.158 0.466	0.757 0.154	1.935 0.022	-0.215 -0.556	
AA598517 Keratin 8 H44051 KERATIN, TYPE I CYTOSKELETAL 14	-0.131 0.020	2.958	-0.156	-0.216	1.840	-0.172	
AA133469 KERATIN, TYPE I CYTOSKELETAL 20	0.381 0.286	0.440 0.322	0.345 0.664	0.437 0.466	0.321 0.312	0.230 -0.087	
AA706022 KERATIN, TYPE II CYTOSKELETAL 1 AA431080 KERATIN, TYPE II CYTOSKELETAL 6D	1.204	0.983	1.163	0.645	0.124	0.739	

			10/0	1004	468	MPI	231	(log base 2 ratio
ACC	Gene Name	ZR75 0.532	YY3 0.572	7Y1 0.221	-0.038	1.158	0.213	(log base 2 ratio
AA485959 AA027012	KERATIN, TYPE II CYTOSKELETAL 7 Kinase insert domain receptor (a type III receptor tyrosine kinase)	0.084	0.844	0.186	-0.032	-0.010	0.469	
	KINESIN HEAVY CHAIN	-0.152	-0.232	0.368	-0.616	0.358	0.164	
	KINESIN LIGHT CHAIN	1.116	0.509	0.685	0.115	0.879	0.370	
H69834	Kininogen	-0.224 0.066	0.335 0.353	0.051 0.155	0.077 0.149	-0.289 0.318	0.635 0.926	
R18845	KRAB zinc finger protein (alternative products)	-0.057	0.466	-0.414	-0.385	0.034	0.178	
AA136710	Lactotransferrin LACTOYLGLUTATHIONE LYASE	0.008	0.226	0.044	0.345	0.025	0.484	
AA496997		-0.381	-0.131	-0.144	0.069	-0.160	0.359	
	Lamin B receptor	-0.175	-0.002 -0.077	-0.004 -0.123	-0.242 0.355	0.143 0.072	0.333 0.587	
	Laminin B1 chain	-0.136 0.058	-0.049	0.321	0.400	0.173	0.433	
AA629897	Laminin receptor (2H5 epitope) Laminin, alpha 2 (merosin, congenital muscular dystrophy)	-0.297	0.109	0.515	0.588	-0.038	0.610	
AA001432	Laminin, alpha 3 (nicein (150kD), kalinin (165kD), BM600 (150kD), epilegrin)	-0.213	0.239	0.582	0.757	0.435	-0.278	
R43734	Laminin, alpha 4	0.448	0.311	0.528	0.483 0.113	0.296 0.238	0.157 0.467	
	Laminin, beta 2 (laminin S)	0.298 -0.045	0.392 -0.240	0.439 0.199	0.819	0.006	0.523	
	Laminin, beta 2 (laminin S) Laminin, gamma 1 (formerly LAMB2)	-0.279	0.144	-0.221	-0.471	0.439	0.449	
H24650 AA101875	LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR	-0.297	-0.407	0.606	-0.226	-0.252	0.280	
AA598629	LARGE PROLINE-RICH PROTEIN BAT3	0.642	0.254	0.327	0.042	0.242	0.091	
R61229	L-arginine:glycine amidinotransferase [human, kidney carcinoma cells, mRNA, 2330 nt]	0.251	0.430 -0.259	0.768 0.113	1.312 0.450	0.325 0.165	0.559 -0.142	
AA504856	Latent transforming growth factor beta binding protein 1	-0.263 -0.615	-0.691	-0.020	0.139	-0.552	0.093	
	Latent transforming growth factor beta binding protein 2 Lecithin-cholesterol acyltransferase	0.559	0.012	0.188	0.110	0.362	0.408	
R06458 AA630328	Lectin, galactoside-binding, soluble, 3 (galectin 3) (NOTE: redefinition of symbol)	-0.056	-0.028	0.352	0.349	0.476	0.488	
AA011057	Lectin, galactoside-binding, soluble, 7 (galectin 7)	0.631	-0.368	0.305	-0.276	-0.175 -0.001	0.285 0.480	
R50354	Leukemia inhibitory factor (cholinergic differentiation factor)	0.319 0.682	0.154 0.371	0.091 0.352	0.184 0.257	0.161	-0.039	
	LEUKOCYTE ELASTASE INHIBITOR	0.503	0.172	0.097	0.473	0.077	-1.121	
	Leukophysin Leukotriene A4 hydrolase	-0.164	0.191	0.091	0.321	-0.295	0.203	
	Ligase I, DNA, ATP-dependent	0.384	0.057	0.215	0.493	-0.308	0.257	
H51404	LIM domain kinase 1	-0.246 0.022	-0.052 0.255	0.278 0.139	0.317 0.343	-0.277 0.030	0.425 0.801	
	Lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	0.445	0.207	0.399	0.589	0.359	0.356	
N68256	Lipase, hepatic Lipoprotein lipase	0.162	0.229	0.416	0.764	0.214	0.481	
AA497029	L-LACTATE DEHYDROGENASE M CHAIN	-0.017	-0.064	-0.214	-0.571	-0.248	0.788	
	Long (electrocardiographic) QT syndrome 2	1.100	-0.220 -0.026	0.648 0.169	0.424 0.376	0.576 -0.203	-0.477 -0.195	
T73556	Long chain fatty acid acyl-coA ligase	0.411 0.154	-0.026	-0.522	0.112	-0.516	0.597	
R68106	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR II C PRECURSOR LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR III-1 PRECURSOR	0.416	0.584	0.887	1.472	0.407	0.524	
H20822	Low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated	0.877	0.312	0.374	0.170	-0.057	1.013	
AA504461	LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR	1.130	0.693	1.180	0.234	0.907	0.669	
T63362	LOWE'S OCULOCEREBRORENAL SYNDROME PROTEIN	1.068	0.50B 0.842	0.339 -0.271	0.312 0.189	0.313 -0.215	-0.257 0.486	
T77636	LPRP	0.188 0.680	0.242	0.399	0.132	0.198	0.351	
T71363 AA669526	L-SERINE DEHYDRATASE	0.114	0.179	0.377	0.006	0.238	0.729	
AA447781		-0.405	0.001	-0.019	-0.375	0.352	0.462	
W73144	Lymphocyte cytosolic protein 1 (L-plastin)	0.278	0.084	0.480	0.677	0.445 -0.003	-0.007 -0.032	
R74169	LYMPHOCYTE-SPECIFIC PROTEIN LSP1	0.160 0.494	0.500 0.261	-0.070 0.095	0.196 0.799	-0.202	-0.178	
W72329	Lymphotoxin alpha (formerly tumor necrosis factor beta) LYMPHOTOXIN-BETA RECEPTOR PRECURSOR	0.236	0.191	0.311	1.359	-0.016	0.928	
H28973	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 1 PRECURSOR	0.338	0.143	0.146	0.149	0.384	1.127	
N62847	Lysosome-associated membrane protein 2 (alternative products)	-0.349	-0.358	-0.252	-0.405	-0.024 -0.011	1.099 0.660	
N63943	Lysozyme	-0.255 -0.465	-0.261 -0.325	-0.097 -0.768	0.360 -0.703	0.424	0.441	
	Lysyl hydroxylase	0.776	0.764	0.602	-0.436	-0.177	0.218	
H01340	Lysyl oxidase Macrophage stimulating 1 (hepatocyte growth factor-like)	-1.096	-0.322	-0.665	-0.885	-0.587	0.743	
T47813	Macrophage stimulating 1 (hepatocyte growth factor-like)	0.947	0.570	0.327	0.583	0.197 0.085	0.358 -1.145	
T51539	Macrophage stimulating 1 (hepatocyte growth factor-like)	-0.247 -0.363	0.313 0.165	-0.151 -0.101	0.075 -0.027	0.253	-0.030	
H86558	MAD protein (MAX-binding protein) MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	-0.416	-0.047	-0.105	-0.317	-0.018	0.340	
AA234897 W56300	MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN MADS	0.614	0.084	0.328	0.459	0.435	0.415	
AA464246	Major histocompatibility complex, class I, C	0.617	0.161	0.433	1.673	0.388	0.454	
H13691	Major histocompatibility complex, class II, DM beta	0.264 2.000	0.309 -0.081	-0.020 2.343	0.040 2.058	0.231 2.134	0.397 -0.385	
AA702254	Major histocompatibility complex, class II, DN alpha	1.390	0.792	0.687	0.789	0.834	0.065	
AA486532	Major histocompatibility complex, class II, DP beta 1 Major histocompatibility complex, class II, DQ beta 1	-0.293	-0.444	-0.042	-0.419	-0.452	0.522	
AA664195	Major histocompatibility complex, class II, DR beta 5	-0.308	0.486	-0.103	0.202	0.474	0.888	
AA227885	Mal, T-cell differentiation protein	0.371	0.187	0.307 -0.665	0.322 -1.607	0.243 -1.094	0.714 0.937	
	MALATE DEHYDROGENASE, CYTOPLASMIC	-0.691 0.805	-0.130 0.157	0.168	0.708	0.353	0.822	
	MALATE OXIDOREDUCTASE Mannose phosphate isomerase	-0.078	0.266	0.396	0.538	0.335	0.390	
	Mannose receptor	-0.355	0.082	-0.288	-0.145	0.287	0.632	
H96213	Mannose-6-phosphate receptor (cation dependent)	0.098	0.539	0.278	0.369 0.162	0.491 0.222	0.580 0.510	
T69284	Mannose-binding lectin, soluble (opsonic defect)	0.354 0.106	0.236 -0.209	0.231 -0.269	-0.267	0.476	0.697	
AA427691	Mannosidase alpha-B (lysosomal) Mannosidase, alpha type II	0.100	1.102	0.046	-0.212	0.579	0.305	
H69561 H47026	Mannosyl(beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	0.537	0.456	0.111	0.291	0.124	-0.326	
H86755	MAP KINASE PHOSPHATASE-1	0.225	0.259	0.170	0.229 0.039	0.200 0.141	0.229 -0.249	
	MATRIN 3	-0.487 -0.425	-0.069 -0.301	-0.216 -0.499	-0.494	-0.731	0.324	
AA155913	Matrix Gla protein	0.460	0.378	0.129	0.179	0.209	0.974	
	Matrix metalloproteinase 1 (interstitial collagenase) Matrix metalloproteinase 10 (stromelysin 2)	0.209	0.087	0.449	0.242	0.070	0.330	
R92994	Matrix metalloproteinase 12 (macrophage elastase)	0.601	0.415	0.241	0.472	0.374	-0.667	
N69322	Matrix metalloproteinase 13 (collagenase 3)	-0.279	0.274 -0.608	0.207 -1.049	-0.011 -0.835	0.279 -1.580	0.110 0.400	
AA443300	Matrix metalloproteinase 2	-1.195 0.678	0.236	0.321	-0.056	0.512	0.033	
T72581	Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) Matrix metalloproteinase 2 (gelatinase A; collagenase type IV)	1.353	0.280	0.376	0.640	0.858	1.514	
AA031514	Matrix metalloproteinase 7 (matrilysin, uterine)	-0.145	-0.077	-0.609	0.072	-0.098	1.183	
N68443	MAX protein	-0.366	-0.166	-0.110	0.238	-0.122 0.450	1.167 0.385	
AA001444	Meis1 (mouse) homolog	0.923 -0.482	0.785 -0.133	0.487 -0.082	0.659 -0.054	-0.042	0.939	
AA463497	Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) Membrane component, chromosome 1, surface marker 1 (40kD glycoprotein, identified by monoclonal	0.184	0.542	-0.738	-0.189	0.155	0.077	
R98936	Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	0.412	0.619	0.003	0.296	0.967	0.926	
N74236	Membrane protein, palmitoylated 1 (55kD)	-0.008	0.275	-0.143	-0.068	0.467 0.042	1.218 1.276	
AA598610	Mesoderm specific transcript (mouse) homolog	0.059 -0.124	0.195 0.390	0.160 -0.184	0.082 -0.438	0.480	0.675	
	Met proto-oncogene (hepatocyte growth factor receptor)	0.369	-0.083	-0.015	0.191	0.310	0.261	
H98666 N80129	Metallopeptidase 1 (33 kD) Metallothionein 1L	0.603	0.398	0.410	0.476	0.655	0.833	
AA670347	7 Metaxin	-0.359	-0.497	0.070	-0.957	-0.436 1.195	1.374 1.144	
AA663793	Methylmalonyl Coenzyme A mutase	1.498 -0.046	0.758 -0.200	0.773 0.101	0.698 -0.138	0.370	0.902	
H08205	Mevalonate kinase MHC class I polypeptide-related sequence A	-0.112	0.043	0.116	-0.112	0.148	0.773	
N71782 AAR4465	MHC class I protein HLA-A (HLA-A28,-B40, -Cw3)	-0.520	-0.211	-0.263	0.035	-0.159	0.668	
T63324	MHC class II DQ alpha	0.572	0.220	-0.094	-0.442 -0.348	-0.342 -0.334	0.812 0.962	
AA45847	MHC class II DQ-beta associated with DR2, DQw1 protein	0.497	-0.001	-0.164	-0.348	-0.534	0.002	

ACC	Gene Name	ZR75	YY3	YY1	468	MPI	231 0.893	(log base 2 ratio
AA158396	MHC class II protein HLA-DO beta chain	-1.448 0.788	-0.443 0.643	-1.198 0.098	-1.116 -0.120	0.061 -0.321	0.981	
AA490920 AA876054	MHC class II transactivator MHC protein HLA-H (hereditary haemochromatosis)	0.083	0.205	0.288	0.416	0.525	0.853	
N67487	Microfibrillar-associated protein 2	0.430 0.294	0.422 0.440	-0.083 0.265	0.177 0.585	0.219 0.276	0.628	
AA496022 N66177	Microfibrillar-associated protein 4 Microphthalmia-associated transcription factor	-0.624	-0.478	-0.087	0.147	-0.101	0.900	
AA863424	MICROSOMAL DIPEPTIDASE PRECURSOR	-0.820	-0.762 0.027	-0.701 0.241	-1.340 0.296	-1.012 0.362	0.863 0.493	
AA421278	Microsomal triglyceride transfer protein (large polypeptide, 88kD) MICROTUBULE-ASSOCIATED PROTEIN 1B	-0.169 -0.450	-0.117	-0.477	-0.710	-0.498	0.444	
	Microtubule-associated protein 4	1.343	-0.195	0.175	0.819	1.063	0.641 0.781	
AA775445	Miller-Dieker syndrome chromosome region	0.875 0.029	0.789 -0.692	1.170 -0.617	-0.026 -0.719	0.754 -0.287	0.701	
AA456608	Mineralocorticoid receptor (aldosterone receptor) Minichromosome maintenance deficient (S. cerevisiae) 3	0.265	0.240	0.075	0.370	0.299	0.012	
AA670357	MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN	0.262 -0.177	-0.037 0.235	-0.016 -0.043	-0.186 -0.184	-0.001 0.417	0.681 0.458	
H05820	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 Mitochondrial carbonic anhydrase	-0.441	-0.343	-0.377	-0.657	-0.474	0.483	
W47015	MITOCHONDRIAL ELONGATION FACTOR TS PRECURSOR	0.267 0.207	0.276 0.166	0.372 0.112	-0.044 0.120	0.154 -0.066	0.285 1.197	
	MITOTIC KINESIN-LIKE PROTEIN-1 Moesin	0.783	0.702	0.795	0.423	0.754	1.488	
R22977 AA011096	Monoamine oxidase A	-0.541	0.014	-0.814	-0.852	-0.756 0.208	2.031 0.932	
AA682423	Monoamine oxidase B	-0.147 0.948	0.147 0.532	-0.300 1.187	-0.210 0.749	1.693	0.376	
AA701476	MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR	0.685	1.382	0.815	0.895	1.273	0.077	
N49725	Mouse double minute 2, human homolog of; p53-binding protein	0.282 -0.020	0.040 0.339	0.257 0.199	0.282 0.092	0.105 0.625	0.518 0.656	
AA448659 R55046	M-PHASE INDUCER PHOSPHATASE 2 MpV17 transgene, murine homolog, glomerulosclerosis	0.750	0.484	0.527	0.384	0.785	1.176	
R33154	Msh (Drosophila) homeo box homolog 1 (formerly homeo box 7)	-0.084 0.223	-0.193 -0.160	-0.003 -0.064	-0.284 -0.034	0.251 -0.312	0.838 0.429	
	Msh (Drosophila) homeo box homolog 2 Mucin 1, transmembrane	0.257	0.216	-0.139	-0.554	-0.274	0.391	
	Mucin 2, intestinal/tracheal	-0.454	-0.659	-0.390	-0.324 0.402	-0.727 D.506	0.509 0.772	
AA159577	Mucin 5, subtype B, tracheobronchial	0.764 0.231	0.651 0.539	0.731 0.408	0.402	0.433	0.591	
AAAAAAAAA	MULTIDRUG RESISTANCE PROTEIN 1 MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 1	-0.304	-0.391	-0.259	-0.106	-0.652	0.910	
AA599158	MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE	0.177 -0.088	-0.109 -0.041	0.006	-0.151 -0.137	-0.001 0.021	1.057 0.132	
N33274	MULTIFUNCTIONAL PROTEIN ADE2 Multiple endocrine neoplasia I	-0.057	-0.346	-0.282	-0.511	-0.229	0.180	
	Murine leukemia viral (bmi-1) oncogene homolog	0.091	-0.538	-0.305	-1.001	-0.958 0.591	-0.129 0.449	
AA176491	Muscle determination factor	0.272 0.054	0.286 -0.364	0.110 -0.101	0.250 -0.246	0.194	0.601	
R77919 AA421718	MUSCLE-SPECIFIC DNASE I-LIKE PRECURSOR MutS (E. coli) homolog 3	-1.004	-0.259	-0.422	-0.411	-0.817	-0.791	
AA443998	MutT (E. coli) human homolog (8-oxo-7,8-dihydroguanosine triphosphatase)	0.533 0.125	0.362 0.656	-0.107 0.135	0.233 0.030	-0.021 -0.363	0.331 1.070	
R92452 N49284	Myasthenic syndrome antigen B [human, fetal brain, mRNA, 3477 nt] MYB PROTO-ONCOGENE PROTEIN	0.241	0.307	0.201	0.988	-0.058	0.132	
H17080	Myelin basic protein	-0.395	-0.315 1.206	-0.224 0.204	0.001 -0.004	-0.514 0.601	0.174 0.462	
	Myeloid cell leukemia sequence 1 (BCL2-related)	0.749 -0.211	-0.471	-0.171	-0.544	-0.341	0.829	
N29376 AA703058	Myeloid cell nuclear differentiation antigen Myeloperoxidase	0.453	0.453	0.097	0.710	0.184	0.700 0.832	
AA282537	MYOCYTE-SPECIFIC ENHANCER FACTOR 2	-0.006 -0.065	-0.166 0.268	-0.085 -0.087	-0.329 -0.319	-0.094 0.024	0.652	
AA283744	MYOCYTE-SPECIFIC ENHANCER FACTOR 2, ISOFORM MEF2 MYOGLOBIN	0.157	-0.220	0.123	-0.135	0.483	0.424	
H90874	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE	0.180	0.550	0.162 -0.559	0.734 -0.892	-0.082 -0.178	0.119 0.782	
T52894	Myosin light chain (alkali) MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM	-0.447 -0.010	0.131 -0.061	-0.159	-0.858	-0.279	-0.136	
AA025850	Myosin VA (heavy polypeptide 12, myoxin)	0.119	0.218	-0.022	0.376	0.164	-0.153 1.039	
AA062993	Myosin VIIA (Usher syndrome 1B (autosomal recessive, severe))	-0.040 0.309	0.347 -0.288	-0.843 0.116	-0.378 -0.458	0.142 0.255	0.524	
AA126989 AA437136	Myosin, heavy polypeptide 11, smooth muscle Myosin, heavy polypeptide 3, skeletal muscle, embryonic	-0.401	0.133	-0.135	-0.321	0.364	0.703	
AA196393	Myosin, light polypeptide 1, alkali; skeletal, fast	0.157 -0.564	0.397 -0.146	0.033 -0.341	-0.106 -0.304	0.254 0.360	-0.278 0.014	
N78927	Myosin, light polypeptide 2, regulatory, cardiac, slow Myosin, light polypeptide 3, alkali; ventricular, skeletal, slow	-0.501	-0.182	-0.088	0.063	0.355	0.134	
AA705225	Myosin, light polypeptide 4, alkali; atrial, embryonic	0.033	-0.203	0.053 0.284	0.505 0.241	0.201 0.490	0.679 0.771	
AA463986	Myosin, light polypeptide 5, regulatory	0.321 -0.080	0.434 0.664	0.248	0.062	0.658	0.565	
AA482231	Myotubular myopathy 1 Myristoylated alanine-rich C-kinase substrate	-0.336	0.268	-0.158	-0.055	0.512 1.069	0.178 0.977	
AA457042	Myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78)	-0.045 -0.007	0.501 0.524	0.136 -0.025	0.294 0.310	0.633	0.432	
AA286908 T68568	Myxovirus (influenza) resistance 2, homolog of murine Na/taurocholate cotransporting polypeptide	0.720	0.528	0.140	0.917	0.445	1.135	
R46823	N-acetylgalactosaminidase, alpha-	0.208 0.064	0.380 0.118	0.172 -0.141	0.265 0.106	0.562 0.269	0.765 0.714	
N77931	N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB N-acetylglucosaminyltransferase I	0.278	0.358	0.106	0.338	0.201	0.491	
AA043796	N-ACETYLLACTOSAMINE SYNTHASE	0.240	0.709	0.733	0.518 0.230	0.273 0.533	-0.418 0.598	
AA455941	N-acylaminoacyl-peptide hydrolase	0.257 0.737	0.354 0.503	0.399	0.458	0.450	0.514	
AA480995	NAD(P)H:menadione oxidoreductase NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE	0.264	0.707	0.324	0.550 0.095	1.431 -0.124	1.014 0.771	
AA922326	NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR	-0.243 -0.019	0.033	-0.091 0.480	0.095	0.357	0.715	
AA458965	NATURAL KILLER CELLS PROTEIN 4 PRECURSOR	1.182	0.490	0.938	0.519	1.372	0.724	
AA133656	Natural resistance-associated macrophage protein 2	0.106 0.061	-0.198 1.295	-0.075 0.164	-0.324 0.166	0.282 0.274	0.175 -0.576	
AA598668 AA609983	N-CHIMAERIN	0.070	1.153	-0.246	0.082	-0.044	0.701	
AA442095	NEDD-4 PROTEIN	0.297	-0.028 0.811	0.014 0.428	-0.391 1.588	0.099 0.895	0.578 0.928	
	Neogenin (chicken) homolog 1 Nerve growth factor beta	0.788 0.097	-0.055	-0.543	-0.499	-0.571	0.811	
T52484 R55303	Nerve growth factor receptor	0.424	0.534	0.194	0.571	0.491	0.893	
	Neuroblastoma RAS viral (v-ras) oncogene homolog	0.146 0.416	-0.236 0.300	0.226 0.526	0.112 0.547	0.254 0.558	0.336 0.072	
AA428960) Neurofibromin 2 (bilateral acoustic neuroma) 3 Neurofilament-66 [human, fetal brain, mRNA, 3197 nt]	0.053	0.132	0.119	-0.020	0.345	0.822	
AA425450	Neuromedin B	0.001 -0.355	0.085 0.116	-0.120 0.141	0.124 0.148	0.520 0.295	1.067 0.622	
	Neuronal pentraxin II NEURON-SPECIFIC X11 PROTEIN	-0.443	-0.206	-0.638	-0.274	0.115	0.772	
H19687 R43817	Neuropeptide Y receptor Y1	0.023	0.257	0.106 -0.107	-0.203 0.078	0.588 0.637	0.730 1.433	
AA46115	7 Neurotrophic tyrosine kinase, receptor, type 1	-0.060 1.416	0.495 0.834	0.107	-0.101	-0.243	0.321	
NEA165	Neurotrophic tyrosine kinase, receptor, type 3 (TrkC) NEUTROPHIL DEFENSINS 1, 2 AND 3 PRECURSOR	-0.053	-0.157	-0.412	-0.394	-0.118	0.564	
AA40097	NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR	0.270 0.248	0.326 -0.136	0.570 0.067	-0.047 -0.403	1.034 -0.101	0.268 0.298	
AA70941	Nidogen (enactin) Niemann-Pick disease, type C1	0.537	0.468	0.253	0.031	0.573	0.376	
AA87784	Nitric oxide synthase 2A (inducible, hepatocytes)	0.449 0.295	0.178 -0.169	0.211 0.527	0.724 0.310	0.361 0.126	0.440 0.407	
AA88496	7 Nitric oxide synthase 3 (endothelial cell) 7 NKG2-C TYPE II INTEGRAL MEMBRANE PROTEIN	1.522	1.212	0.347	1.326	1.271	0.461	
AA39781	9 NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN	0.000	0.146 0.883	-0.092 -0.320	0.158 -0.027	0.055 -0.046	-0.477 0.451	
AA70165	2 NKG5 PROTEIN PRECURSOR N-methylpurine-DNA glycosylase	0.148 -0.076	0.883	-0.294	-0.411	-0.311	0.390	
N26769 R52824	N-MYC PROTO-ONCOGENE PROTEIN	0.145	0.883	0.719	0.082 -0.589	0.497 -0.487	0.665 0.109	
AA28021	4 Non-catalytic region of tyrosine kinase 8 Non-metastatic cells 2, protein (NM23B) expressed in	-0.468 0.830	-0.218 0.454	-0.270 0.634	0.406	0.439	0.109	
AA49002	O 1401-1116-08-04-08-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-							

	Gene Name Non-specific cross reacting antigen	ZR75 0.363	YY3 0.068	YY1 -0.192	468 -0.327	MPI -0.052	231 0.055	(log base 2 ratio
AA670439	Nomie disease (pseudoglioma) protein	1.037 0.082	0.436 0.858	0.349 -0.022	0.242 0.519	1.253 0.295	0.892 0.151	
AA629687 R55220	Nr12 N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG	0.513	0.304	0.197	0.048	0.282	0.407	
AA447482	Nuclear antigen Sp100	-0.437	-0.508 -0.139	-0.489 0.179	-0.583 -0.089	-0.489 0.445	0.088	
	Nuclear autoantigenic sperm protein (histone-binding) Nuclear cap binding protein, 80kD	-0.104 -1.109	-0.138	-0.549	-0.880	-1.212	1.068	
AA406269	Nuclear factor I/X (CCAAT-binding transcription factor)	0.192	0.297	-0.054	-0.023	0.138	0.533	
AA451716	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	-2.080 -0.814	-1.471 0.070	-1.754 -0.204	-1.543 0.095	-1.559 0.134	0.186	
AA401428	NUCLEAR FACTOR RIP140 NUCLEAR PORE COMPLEX PROTEIN NUP214	0.524	0.707	0.206	0.803	0.527	0.364	
AA412691	Nuclear transcription factor Y, alpha	0.940 -0.209	0.285 0.117	0.471 -0.063	0.278 0.229	0.759 0.373	0.456 1.512	
	NUCLEAR TRANSPORT FACTOR 2 NUCLEOBINDIN PRECURSOR	0.237	0.247	0.117	-0.175	0.143	1.190	
	NUCLEOLAR TRANSCRIPTION FACTOR 1	0.335	0.348	0.039 -0.165	0.242 -0.272	0.536 0.283	1.058 0.460	
	NUCLEOLIN	0.235 -0.530	0.190 -0.125	-0.232	-0.352	0.244	0.342	
	NUCLEOLYSIN TIA-1 Nucleophosmin (nucleolar phosphoprotein B23, numatrin)	-0.177	0.125	0.251	0.043	0.314	0.246	
AA644092	NUCLEOSIDE DIPHOSPHATE KINASE A	0.492 0.670	-0.168 0.328	0.154 0.257	-0.128 0.296	-0.152 0.387	1.214 0.820	
	Nucleoside phosphorylase Oligodendrocyte myelin glycoprotein	1.581	0.386	0.985	0.540	1.441	0.988	
R31938	Opioid receptor, kappa 1	-0.120 0.107	0.178 0.547	-0.346 -0.079	-0.259 0.108	-0.294 0.381	0.852 0.718	
	Opioid-binding cell adhesion molecule Ornithine aminotransferase (gyrate atrophy)	-1.863	-1.364	-1.240	-1.459	-1.576	0.467	
	Ornithine decarboxylase 1	-0.718	-0.470	-0.318	-0.378 -0.226	-0.184 0.487	0.825 0.815	
	Orosomucoid 1	-0.343 -0.147	-0.277 0.036	0.226 -0.459	-0.226	-0.027	1.002	
H68838 H23979	ORPHAN RECEPTOR TR2 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR	0.436	1.071	0.561	0.708	0.361	0.942	
H80138	Oxoglutarate dehydrogenase (lipoamide)	2.045 -0.063	0.588 0.018	0.791 -0.019	1.063 0.348	0.845 0.375	0.736 0.788	
	Oxytocin receptor P glycoprotein 3/multiple drug resistance 3	0.587	-0.331	-0.116	-0.249	-0.197	-0.365	
AA456432	PPROTEIN	0.607 0.554	0.944	-0.203 -0.092	0.834 0.795	0.158 0.723	-0.067 0.429	
	P55-C-FOS PROTO-ONCOGENE PROTEIN	-0.103	0.154	-0.249	0.005	0.073	0.412	
W88740	P68 PROTEIN P80-COILIN	0.137	0.010	0.884	0.461	0.094	0.588	
AA856874	Paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein)	0.551 -0.042	0.307 -0.024	0.350 0.159	0.233 0.255	0.244 0.465	0.998 0.319	
	Paired basic amino acid cleaving system 4 Paired box homeotic gene 6 (aniridia, keratitis)	0.632	0.226	0.456	0.171	0.513	-1.118	
AA844998	Pancreatic polypeptide	-0.606	-0.301	-0.175 0.355	-0.439 0.470	-0.062 -0.046	0.297 0.731	
	Pantophysin [human, keratinocyte line HaCaT, mRNA, 2106 nt]	0.223 0.568	0.198 0.477	0.404	0.504	0.403	0.692	
R12373 R11526	Paraoxonase 1 Parathymosin	0.146	0.159	-0.090	-0.223	0.758	-0.438 -0.177	
W37306	Parathyroid hormone	0.031 -0.009	0.435 0.108	0.660 0.064	0.039 0.120	0.680 0.535	-0.177	
	Parathyroid hormone receptor 1 Parathyroid hormone-like hormone	0.607	1.242	0.263	0.278	1.151	-0.625	
AA010609	Parvalbumin	-0.535 -0.229	-0.305 0.073	0.008	-0.572 0.281	0.284 -0.482	0.519 0.679	
	Patched (Drosophila) homolog PBX1a and PBX1b	0.230	0.253	0.417	-0.050	-0.156	-0.054	
	PCTAIRE protein kinase 3	-0.605	-0.236	-0.156	-0.258	0.062 0.355	-0.780 0.313	
R72097	PEPSINOGEN A PRECURSOR	0.620 -0.390	0.580 -0.287	-0.081 -0.313	0.327 -0.602	-0.627	0.277	
D66310	Peptidase D Peptidylglycine alpha-amidating monooxygenase	-0.030	0.320	-0.137	-0.009	0.097	0.416 0.503	
AA401291	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR	0.303 -0.306	-0.040 -0.155	-0.240 0.162	-0.243 -0.076	-0.160 0.435	-0.386	
AA481464 AA676404	Peptidylprolyl isomerase B (cyclophilin B) Peptidylprolyl isomerase C (cyclophilin C)	0.386	-0.024	0.198	-0.207	0.341	0.016	
R26732	Peripheral myelin protein 22	0.432 -0.193	0.781 0.022	0.303 0.173	0.124 0.110	0.556 0.107	0.307 0.743	
AA455945 H10965	PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR Peroxisomal biogenesis factor 12	0.139	0.493	0.302	-0.008	0.327	0.510	
AA234671	Peroxisomal membrane protein 1 (70kD, Zellweger syndrome)	-0.017	0.625	0.128 0.082	-0.396 0.080	0.238 0.458	0.428	
AA452566	Peroxisomal membrane protein 3 (35kD, Zellweger syndrome) Phenylethanolamine N-methyltransferase	-0.041 0.214	0.055 -0.259	0.062	-0.060	-0.080	0.336	
N63192 W37864	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	0.221	-0.109	0.221	-0.022	0.362 0.766	0.129 0.568	
AA486200	Phosphate carrier, mitochondrial	-0.080 -0.322	0.000 -0.281	0.216 -0.015	-0.263 0.129	-0.333	0.554	
R89808 W72473	PHOSPHATIDYLINOSITOL PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM	0.795	0.455	0.441	0.728	0.629	0.801	
AA191461	Phosphatidylinositol 3-kinase p110 beta isoform	0.012	0.037 0.279	0.166 -0.289	-0.180 -0.332	-0.003 0.260	-0.253 0.165	
AA464176	Phosphatidylinositol 3-kinase, catalytic, gamma polypeptide PHOSPHATIDYLINOSITOL 4-KINASE ALPHA	0.369	0.696	0.180	0.538	0.855	0.423	
AA424735	Phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria)	0.431	0.754	0.095 0.285	0.025 0.117	0.991 0.245	0.325 0.049	
AA098979	Phosphatidylinositol glycan, class F PHOSPHATIDYLSERINE SYNTHASE I	0.579 -0.223	1.093 0.268	0.263	-0.015	-0.068	0.119	
H28984 AA453293	Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)	-0.074	-0.014	0.141	-0.150	0.582	0.340	
W92514	Phosphodiesterase 6A, cGMP-specific, rod, alpha	-0.214 -0.291	-0.249 -0.142	-0.437 0.124	-0.397 -0.069	-0.268 -0.002	0.046 0.376	
AA074148	Phosphodiesterase 6G, cGMP-specific, rod, gamma Phosphoenolpyruvate carboxykinase 1 (soluble)	0.774	0.113	0.080	-0.185	-0.235	0.332	
W72140	Phosphofructokinase (liver type)	0.960	0.360 0.027	0.235 0.189	0.306 -0.075	0.725 0.498	0.174 0.465	
	Phosphofructokinase, muscle	0.363 -0.955	-0.060	-0.574	-0.403	-0.466	0.412	
AA488373	Phosphofructokinase, platelet Phosphoglucomutase 1	-0.440	0.581	-0.126	-0.092	0.208	0.101 0.718	
AA598759	Phosphogluconate dehydrogenase	0.107 0.642	0.271 -0.547	-0.396 0.296	-0.032 0.019	0.103 -0.797	0.481	
AA599187	Phosphoglycerate kinase 1 Phosphoglycerate mutase 1 (brain)	-0.181	0.040	0.267	-0.086	0.527	1.276	
N45318	Phosphoglycerate mutase 2 (muscle)	-0.205 -0.024	0.256 0.299	-0.187 -0.232	-0.194 0.002	-0.089 0.584	0.644 0.216	
	Phospholipase C. beta 4	0.480	0.559	0.193	-0.175	-0.034	0.092	
H22563 H57180	Phospholipase C, gamma 2 (phosphatidylinositol-specific)	0.345	0.465	0.296	-0.042	-0.081 -0.036	0.256 0.696	
AA454856	Phospholipid hydroperoxide glutathione peroxidase	0.884	0.473 0.011	0.607 0.318	0.050 0.406	-0.169	0.900	
AA156863 N35888	Phosphomannomutase Phosphomannomutase 2	0.468	0.087	0.333	0.289	0.096	0.693	
A A 4 E 4 4 B B	Phosphorihosyl pyrophosphate synthetase 2	0.254 0.157	0.654 0.621	0.038 0.110	0.208 0.165	0.970 0.831	0.305 0.498	
AA598487	Phosphoribosyldycinamide formyltransferase, phosphoribosyldycinamide synthetase, phosphoribosylt Phosphorylase kinase, alpha 2 (liver), glycogen storage disease IX	0.343	0.052	0.100	0.108	0.092	0.428	
AA201732	Phosphorylase kinase, gamma 2 (testis)	0.245	0.315	-0.197	0.591 0.100	0.846 0.330	0.351 0.377	
AA147640	Phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	0.317 0.751	-0.072 0.390	0.313 0.685	0.100	1.005	0.470	
A A 447730	Pigment epithelium-derived factor Pim-1 oncogene	0.374	0.260	0.430	-0.124	-0.077	-0.176	
AA130714	Placental growth factor, vascular endothelial growth factor-related protein	0.013 0.839	-0.031 0.599	-0.217 0.883	0.139 0.742	-0.190 0.394	-1.033 0.297	
H03346 T72076	PLACENTAL PROTEIN 11 PRECURSOR PLASMA RETINOL-BINDING PROTEIN PRECURSOR	0.430	0.698	0.544	0.586	0.392	0.458	
T69450	PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1	0.389	0.307 0.692	0.025 0.204	0.316 0.169	0.388 0.667	0.676 0.474	
T73090	Plasminogen Plasminogen activator inhibitor, type I	0.284 0.341	0.692	0.362	-0.104	0.004	-0.318	
N54794 T49159	Plasminogen activator inhibitor, type II (arginine-serpin)	0.121	0.680	0.068	0.173	1.299 -0.040	-0.249 0.155	
AA447797	Plasminogen activator, tissue type (t-PA)	0.077 0.153	0.503 1.079	0.221 0.509	-0.010 0.417	0.125	0.193	
AA454879 T67549	Plasminogen activator, urokinase receptor Plasminogen-like protein	-0.503	0.431	0.089	-0.102	-0.082	0.381	

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ACC	Gene Name Plastin 1 (I isoform)	ZR75 0.328	YY3 0.216	YY1 0.668	468 0.652	MPI 0.297	0.506	(log base 2 ratio
T97181	Platelet factor 4	0.281 -0.316	0.816 -0.398	-0.016 -0.073	0.010 -0.057	0.938 -0.121	0.865 0.987	
R22412 T49540	Platelet/endothelial cell adhesion molecule (CD31 antigen) Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	0.634	0.289	0.207	-0.023	0.674	0.804	
AA701502	Platelet-derived growth factor PDGF-A	0.045 0.141	0.239 -0.595	0.721 -0.245	-0.171 -0.039	0.256 -0.111	-0.107 0.606	
R56211 AA001449	Platelet-derived growth factor receptor, beta polypeptide Pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	0.819	0.705	0.631	0.116	1.295	0.438 0.830	
N67770	PMEL 17 PROTEIN PRECURSOR	0.063 0.543	-0.090 0.136	-0.085 0.555	-0.135 0.332	0.304 0.417	0.830	
R84893 AA429661	Polycystic kidney disease 1 (autosomal dominant) Polymerase (DNA directed), delta 1, catalytic subunit (125kD)	0.059	-0.075	0.190	-0.174	0.048	0.826	
AA479052	Polymerase (RNA) If (DNA directed) polypeptide A (220kD)	0.458 -1.019	0.432 -1.621	0.313 -1.077	-0.083 -1.549	0.484 -1.085	0.628	
H99681 AA677517	POLYPOSIS LOCUS PROTEIN 1 Polypyrimidine tract binding protein (hnRNP I) {alternative products}	1.613	0.860	0.853 -0.682	0.488 -0.702	0.892 -0.412	-0.018 0.555	
N30302	POSSIBLE GTP-BINDING PROTEIN HSR1 POTASSIUM CHANNEL PROTEIN KV1.1	0.061 0.723	-0.312 -0.416	-0.479	-0.706	-0,423	0.855	
H38522	POU domain, class 2, transcription factor 1	-0.672 0.750	-0.044 0.578	0.020 0.218	-0.134 0.535	-0.070 0.641	0.967 0.889	
AA873635 N63968	POU domain, class 2, transcription factor 2 POU homeobox protein	-0.572	-0.534	-0.124	-0.442	-0.010	0.604	
AA677388	Pre-alpha (globulin) inhibitor, H3 polypeptide	0.443 0.940	0.243 0.589	0.346 0.138	0.089	0.489 0.792	0.287 0.047	
T59641 AA778198	PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-2 PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-3	-0.461	-0.077	-0.236	0.009	0.260	0.970	
W51985	Pregnancy specific beta-1 glycoprotein 5	0.568 0.561	0.246 -0.012	0.481 0.110	0.240 0.132	0.687 0.123	0.781 0.551	
W84789 N32768	Pregnancy-associated plasma protein A Pregnancy-specific beta 1-glycoprotein 7	0.639	0.379	0.142	-0.248	0.622 -0.083	0.627 0.263	
R73909	Pregnancy-specific beta-1 glycoprotein 13	0.065 1.083	-0.334 0.815	-0.178 0.427	0.360 0.260	0.548	0.180	
N30553 R70868	Pregnancy-specific beta-1 glycoprotein 4 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN E PRECURSOR	1.122	0.644	-0.431	0.283 -0.147	-0.201 0.202	0.359	
N33827 T65786	PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT PRECURSOR PRE-MRNA SPLICING FACTOR SF2, P33 SUBUNIT	0.300 0.234	0.331 0.313	0.075 -0.247	0.003	0.073	-0.224	
AA598400	PRE-MRNA SPLICING FACTOR SRP20	-0.237 0.451	0.347 0.547	-0.453 -1.196	-0.234 0.008	0.059 0.194	-0.362 0.070	
AA496787 N54494	PRE-MRNA SPLICING FACTOR SRP75 Prepro-plasma carboxypeptidase B	0.451	0.092	-0.005	0.488	0.425	0.217	
AA411814	Presenilin 1 (Alzheimer disease 3)	0.248 0.540	0.249 0.443	-0.297 0.094	-0.080 -0.195	0.358 0.887	0.490 0.832	
AA450249	Presenilin 2 (Alzheimer disease 4) Prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal fam	0.547	0.565	-0.247	0.301	0.484	-0.203	
R02740	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74	0.547 0.199	0.232	0.278 -0.079	0.304 0.119	0.283 0.187	0.075 -0.007	
T62636 AA115309	PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR	-0.613	-0.510	-0.202	-0.644	0.091	-0.711	
AA916325	PROBABLE TRANS-1,2-DIHYDROBENZENE-1,2-DIOL DEHYDROGENASE	0.371 0.994	1.039 0.812	-0.341 0.336	0.455 0.323	-0.255 0.568	0.432 0.190	
AA291742 AA443908	Probable transcription factor PML (alternative products) PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE	-0.153	-0.119	-0.013	0.442	-0.031 1.181	0.350 0.501	
N30191	PROCHOLECYSTOKININ PRECURSOR	1.911 0.301	0.468 0.256	1.227 0.594	0.607 0.373	0.674	-0.326	
A A 4 E 7 C 7 1	Procollagen C-endopeptidase enhancer Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide	0.406	0.294	0.406	0.017 0.451	0.613 0.143	-0.707 -0.510	
AA426212	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein di	0.855 0.153	1.496 0.380	-0.152 0.153	0.394	0.548	-0.367	
AA040703 AA402883	Progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial a	0.734	0.588 0.750	0.447	0.543 0.277	0.609 0.666	0.427 0.361	
AA521466 R63647	Programmed cell death 2 Prolactin receptor	0.500 0.401	0.750	0.327	0.389	0.487	0.402	
AA450265	Proliferating cell nuclear antigen	0.510 0.550	0.382 -0.165	0.106 0.264	-0.081 0.275	0.682 -0.117	-0.039 0.396	
N50854	PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 Proliferation-associated gene A (natural killer-enhancing factor A)	0.204	0.109	0.180	0.231	0.280	0.210	
AA434067	Proline arginine-rich end leucine-rich repeat protein	0.838	0.611 0.192	0.434 0.190	0.261	0.659 0.514	-0.493 0.469	
AA664056 AA446316	Prolyl endopeptidase Proopiomelanocortin (adrenocorticotropin/ beta-lipotropin/ alpha-melanocyte stimulating hormone/ beta-	0.329	-0.149	0.001	-0.261 0.874	0.501 0.218	0.210 -0.297	
H52256	Properdin P factor, complement Propionyl Coenzyme A carboxylase, beta polypeptide	0.480 1.777	0.686 1.196	0.292 0.434	0.874	1.003	-0.983	
R46700 AA608575	Propionyl-coA carboxylase alpha chain	-0.215	0.350 0.545	-0.362 0.558	-0.166 0.956	0.527 0.393	-0.312 0.247	
R42630 AA069517	Proprotein convertase subtilisin/kexin type 1 Proprotein convertase subtilisin/kexin type 2	0.502 0.563	-0.116	-0.023	-0.287	0.562	0.052	
T53298	Prostacyclin-stimulating factor [human, cultured diploid fibroblast cells, mRNA, 1124 nt]	0.221 0.303	0.467 0.194	0.055 0.345	-0.073 -0.082	0.991 0.305	0.271 0.115	
AA406362	Prostaglandin E receptor 2 (subtype EP2), 53kD Prostaglandin E receptor 3 (subtype EP3) (alternative products)	-0.394	0.240	-0.465	0.169	0.433	0.139	
AAA54668	Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.446 0.131	-0.326 0.358	-0.274 -0.169	-0.240 -0.100	-0.714 0.196	-0.747 0.370	
AA490981	Prostate specific antigen	0.108	0.374	0.750 0.547	0.054 0.347	0.386 0.238	0.022 0.576	
N64840	PROSTATE-SPECIFIC MEMBRANE ANTIGEN Prostatic binding protein	0.137 0.992	-0.043 0.800	0.625	0.553	1.194	0.007	
T72361	Protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin	0.197 -0.218	0.403 0.191	0.143 0.094	0.006 0.036	0.451 -0.086	0.015	
AA284528	Protease, serine, 2 (trypsin 2) Proteasome (prosome, macropain) subunit, beta type, 5	0.240	0.065	0.224	-0.037	0.432	0.311	•
AA070997	Proteasome (prosome, macropain) subunit, beta type, 6	-0.342 0.355	-0.422 0.434	-0.234 0.226	-0.324 0.162	-0.393 0.962	-0.522 -0.192	
AA862434 AA181300	PROTEASOME CHAIN 7 PRECURSOR PROTEASOME COMPONENT C13 PRECURSOR	0.342	-0.124	0.181	-0.298	-0.057	0.722	
R27585	Proteasome component C2 Proteasome component C5	-0.441 1.021	-0.453 0.599	-0.251 0.210	-0.184 0.333	-0.538 0.297	0.419 -0.176	
T68758 AA465237	PROTEASOME COMPONENT C8	0.079	-0.018 -0.580	-0.320 -0.523	-0.419 -0.112	-0.065 -0.716	0.478 -0.633	
AA116060 T54166	PROTEASOME COMPONENT C9 PROTEASOME COMPONENT MECL-1 PRECURSOR	-0.412 -0.242	0.189	-0.303	-0.161	0.150	-0.814	
AA047338	PROTEASOME IOTA CHAIN .	-0.217 0.035	0.286 0.176	0.089 -0.257	0.103 -0.315	0.474	0.735 0.362	
AA598815	i PROTEASOME ZETA CHAIN Protective protein for beta-galactosidase (galactosialidosis)	-0.201	-0.242	0.214	-0.031	0.005	0.377	
AA703141	PROTEIN 4.1	0.612 0.275	-1.090 0.130	0.384 -0.041	0.391 0.174	0.002 -0.215	-0.098 -0.608	
W86431 AA496810	Protein C inhibitor) Protein kinase C substrate 80K-H	0.249	0.257	-0.118	0.071	0.816	0.150	
AA029890	Protein kinase C, alpha	-0.349 -0.259	-0.519 0.133	-0.675 -0.014	-0.318 0.211	0.126 -0.200	0.750 0.436	
AA479102 AA496360	Protein kinase C, beta 1 PROTEIN KINASE C, DELTA TYPE	0.882	-1.091	0.152	0.638 -0.228	-0.490 -0.589	0.466 0.332	
R89715	Protein kinase C, gamma Protein kinase C, iota	-0.227 -0.374	-0.633 -0.447	-0.119 -0.471	0.186	-0.495	-0.483	
T57875 N53380	Protein kinase C, mu	0.589	0.550 -0.064	0.273 0.096	0.347 0.384	0.370 0.144	-1.042 -0.285	
H60824	PROTEIN KINASE C, THETA TYPE Protein kinase C, zeta	0.375 -0.201	0.234	0.864	0.893	-0.174	0.363	
AA28166	7 Protein kinase inhibitor [human, neuroblastoma cell line SH-SY-5Y, mRNA, 2147 nt]	-0.919 0.162	-0.531 0.573	-0.048 -0.045	-0.207 -0.345	-0.383 0.161	0.516 0.023	
W68141	Protein kinase, cAMP-dependent, catalytic, alpha Protein kinase, cAMP-dependent, catalytic, beta	0.613	0.659	0.620	0.471	0.598	-0.083	
AA48536	Protein kinase, cAMP-dependent, regulatory, type I, beta	-0.126 0.190	0.139 0.038	-0.111 0.087	-0.271 0.040	-0.339 0.671	-0.268 0.237	
AA01007	7 Protein kinase, cAMP-dependent, regulatory, type II, beta 9 Protein kinase, interferon-inducible double stranded RNA dependent	-0.131	0.288	0.011	0.133	-0.233	0.429	
AA44398	Protein phosphatase 1, catalytic subunit, alpha isoform Protein phosphatase 1, catalytic subunit, beta isoform	0.165 0.222	0.337	0.537 0.137	0.065 0.447	0.366 0.129	0.383	
R26186 AA59909	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	0.616	0.339	0.016 -0.189	0.012 -0.185	0.742 -0.406	-0.579 0.215	
1100407	Protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform 3 Protein phosphatase 2 (formerly 2A), regulatory subunit B" (PR 72), alpha isoform and (PR 130), beta i	0.026 0.072	0.432	-0.169	0.118	-0.193	0.836	
14/26270	Protein phosphatase 24, regulatory subunit 8' albha-1	-0.243 0.226	-0.017 0.173	-0.110 0.265	0.381 0.109	0.278 0.353	0.901 1.102	
AA68263	1 Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)/alternative p	5.225						

		ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
ACC Get	ne Name otein phosphatase 4 (formerly X), catalytic subunit	0.590	0.341	-0.098	0.021	0.693	0.855	(log bass 2 lane
AA428335 PR	ROTEIN PHOSPHATASE INHIBITOR 2	0.131	0.546 0.252	0.129 0.133	0.491 -0.018	0.954 0.817	0.723 0.743	
AA427433 PR	NOTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, ALPHA ISOFORM ROTEIN PHPS1-2	0.111 -0.347	-0.143	-0.347	-0.344	0.524	0.983	
AA099140 Pro		-0.108	-0.002	0.219	-0.169	-0.194 0.809	0.278 0.812	
AA496013 Pro	otein serine/threonine kinase stk2 ROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT	0.205 0.334	0.137 -0.141	-0.016 0.179	-0.438 0.356	0.182	0.839	
H73928 PR R06605 Pro	otein tyrosine phosphatase, non-receptor type 1	0.009	0.420	0.317	0.441	0.129	0.627	
AA446259 Pro	otein tyrosine phosphatase, non-receptor type 12	0.267 0.324	0.413 -0.042	0.184 0.088	-0.285 0.061	0.860 0.432	0.852 0.788	
AA428195 Pro	otein tyrosine phosphatase, non-receptor type 2 otein tyrosine phosphatase, non-receptor type 3	0.346	0.156	0.017	0.346	0.466	0.419	
AA262719 Pro	otein tyrosine phosphatase, non-receptor type 7	0.153	0.027	0.297	0.392 0.235	-0.085 0.134	0.517 0.865	
AA434420 Pro	otein tyrosine phosphatase, non-receptor type 9	-0.242 -0.143	0.018 0.189	0.166 0.252	0.248	0.347	-0.063	
H82419 Pro H18633 Pro	otein tyrosine phosphatase, receptor type, alpha polypeptide otein tyrosine phosphatase, receptor type, beta polypeptide	0.395	0.357	0.050	-0.142	0.560	0.354	
H74265 Pro	otein tyrosine phosphatase, receptor type, c polypeptide	-0.381 0.035	-0.112 0.339	-0.030 -0.068	0.177 0.021	-0.100 -0.180	-0.283 0.529	
R14294 Pro	otein tyrosine phosphatase, receptor type, delta polypeptide otein tyrosine phosphatase, receptor type, f polypeptide	0.496	0.551	0.414	-0.301	0.991	0.804	
R38343 Pro	otein tyrosine phosphatase, receptor type, gamma polypeptide	-0.302	0.157	0.147 0.238	0.067 0.017	0.075	-0.235 0.541	
	otein tyrosine phosphatase, receptor type, mu polypeptide	-0.033 0.485	0.425 0.472	-0.149	0.020	0.245	0.563	
AA496902 PR AA453789 Pro	otein-tyrosine kinase 7	-0.318	-0.183	-0.217	-0.307	0.380 0.747	0.285 0.711	
AA173454 Pro	otein-tyrosine kinase RON	0.655 0.412	0.950 0.353	0.123 -0.021	-0.041 0.108	0.175	0.739	•
AA482128 Pro R45056 PR	otein-tyrosine kinase tyk2 (non-receptor) ROTEIN-TYROSINE PHOSPHATASE 2C	0.717	0.102	0.097	0.338	0.484	0.577	
AA476461 PR	ROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR	0.968 1.096	0.149 1.111	0.323 0.430	0.276 0.430	-0.744 1.080	0.202 0.328	
R45264 Pro	oteolipid protein (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated) ROTHROMBIN PRECURSOR	0.734	0.753	0.022	0.204	0.442	0.717	
AA442991 Pro	othymosin alpha	0.706	0.095	0.503	0.674 -0.206	0.312 0.560	0.607 0.539	
AA425746 Pro	oto-oncogene AML1 (alternative products)	0.383	0.444 0.484	0.179 0.180	0.311	0.254	0.182	
H05800 PR	oto-oncogene c-cot (protein-serine/threonine kinase) ROTO-ONCOGENE DBL PRECURSOR	0.234	-0.054	-0.514	-0.789	-0.060	0.480	
AA469965 PR	ROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK	0.737 -0.010	0.683 0.040	0.545 0.045	0.250 0.091	0.457 0.397	0.122 0.532	
AA151249 Pro	otoporphyrinogen oxidase rB-ASSOCIATED SPLICING FACTOR	0.599	0.547	0.093	0.146	0.202	-0.004	
T65772 pul	ulmonary surfactant protein (SP5)	-0.531	0.275	-0.288	-0.360	0.274 0.018	0.475 0.432	
T65772 pul	Ilmonary surfactant protein (SP5)	0.390 0.589	0.233 0.668	0.096 0.171	0.183 0.572	0.471	0.446	
AA487267 PU	ULMONARY SURFACTANT-ASSOCIATED PROTEIN A PRECURSOR UTATIVE 60S RIBOSOMAL PROTEIN	0.670	0.586	0.123	0:167	0.275	-0.297	
AA476272 PU	LITATIVE DNA BINDING PROTEIN A20	1.017 -0.593	0.110 -0.270	0.181 0.036	0.044 -0.370	0.287 -0.490	-0.226 0.198	
H48494 PU	UTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE UTATIVE INSULIN-LIKE GROWTH FACTOR II ASSOCIATED PROTEIN	0.011	0.656	0.050	0.104	-0.217	0.243	
AA598561 PU	UTATIVE MUCIN CORE PROTEIN PRECURSOR 24	-0.715	-0.420	-0.164	-0.354 0.024	-0.770 0.014	0.307 -0.369	
AA706929 PU	UTATIVE PROTEIN PHOSPHATASE 2C	-0.087 0.150	0.079 0.122	0.090 -0.304	0.024	-0.672	0.846	
AA053393 PU H09721 PU	UTATIVE RECEPTOR PROTEIN UTATIVE SERINE/THREONINE-PROTEIN KINASE P78	-0.215	-0.026	-0.423	-0.579	-0.320	0.688	
T77729 Pv	vruvate carboxylase	0.471 0.062	0.317 0.563	0.424 -0.142	0.326 -0.212	0.115 -0.070	0.275 0.554	
T65758 Py	yruvate dehydrogenase (lipoamide) alpha 1 yruvate dehydrogenase (lipoamide) beta	0.323	0.401	0.057	-0.168	0.480	-0.351	
AA169469 Py	yruvate denydrogenase kinase, isoenzyme 4	1.775	0.633	0.893 -0.686	0.824 -0.600	0.603 -0.423	-0.178 0.778	
R08829 Py	yruvate kinase, liver	-0.516 0.702	-0.389 0.474	0.070	-0.250	0.604	0.575	
AA490938 Qu T82414 RA	uinone oxidoreductase (NQO2) AB2, member RAS oncogene family	0.565	0.781	0.165	0.213	0.511	0.598	
H51113 RA	AB3A, member RAS oncogene family	-0.225 0.511	-0.668 0.312	-0.656 0.318	-0.484 0.109	-1.188 0.513	0.578 0.557	
W44889 RA N53449 RA	AB6, member RAS oncogene family AD52 (S. cerevisiae) homolog	-0.695	-0.118	-0.629	-0.486	-0.154	0.591	
	adin blood group	0.453	1.309 0.768	-0.954 -0.052	0.710 -0.082	0.767	0.599 0.765	
AA479781 Ra	adixin AG (recombination activating gene) cohort 1	0.470 -0.063	0.708	-0.052	0.072	0.288	0.466	
	AN binding protein 1	-1.080	-0.281	-0.422	-0.502	-0.350 0.326	0.995 0.527	
AA682897 RA	AP1, GTPase activating protein 1	0.606 0.319	0.232 0.655	0.218 -0.054	0.094 -0.080	0.172	0.657	
AA279804 RA	AP1A, member of RAS oncogene family AS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1	-0.019	-0.254	-0.187	0.033	-0.916	0.545	
R76314 Ra	as homolog gene family, member G (rho G)	-0.332 0.389	0.252 0.777	-0.104 0.204	0.015 0.381	0.341 0.619	0.417 0.821	
	AS-LIKE PROTEIN TC21 as-related C3 botulinum toxin substrate 2	0.211	0.587	0.005	0.051	0.186	0.208	
	AS-RELATED PROTEIN RAB-1A	0.510	0.290 0.535	0.057 -0.011	0.372 0.029	0.433 -0.277	0.350 0.624	
	AS-RELATED PROTEIN RAB-4A AS-RELATED PROTEIN RAB-5A	-0.021 -0.140	0.333	-0.016	0.322	0.301	0.444	
	AS-RELATED PROTEIN RAD-SA AS-RELATED PROTEIN RAL-A	0.238	0.420	0.290	0.514	0.701	0.419	
AA487526 Re	eceptor protein-tyrosine kinase EDDR1	2.354 0.411	2.035 0.035	0.156 0.167	0.691 0.107	1.904 0.179	0.877 0.768	
AA074224 Re	ecO protein-like (DNA helicase Q1-like)	0.116	0.507	0.053	0.218	0.090	0.611	
AA625655 Re	egenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein)	0.788 0.578	0.691 0.163	0.805 -0.232	0.352 0.529	0.977 0.189	0.945 0.357	
AA017544 Re	tegulator of G-protein signalling 1 tegulator of nonsense transcripts 1	0.539	-0.014	-0.226	0.091	0.224	0.899	
AA458630 RE	ENIN PRECURSOR, RENAL	0.031	0.318	0.029	0.279	0.937 0.405	0.654 0.401	
	teplication factor C (activator 1) 1 (145kD)	-0.372 -0.476	0.259 -0.172	-0.093 -0.218	-0.043 -0.182	0.899	0.669	
N93924 Re	teplication factor C, 37-kD subunit teplication protein A (E coli RecA homolog, RAD51 homolog)	-0.100	0.130	0.105	0.087	0.359	0.567	
H59259 Re	teplication protein A (E coli RecA homolog, RAD51 homolog)	-0.374 -0.177	0.189 0.337	-0.136 0.125	-0.026 0.353	0.653 0.695	0.629 0.345	
R39861 Re	teplication protein A2 (32kD) testin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	-0.139	0.291	0.142	0.126	0.638	0.724	
H24956 R	tet proto-oncogene (multiple endocrine neoplasia MEN2A, MEN2B and medullary thyroid carcinoma 1	0.300	0.718	0.152	0.267 -0.173	0.741 0.332	0.496 0.157	
H84114 R	tetinal outer segment membrane protein 1	-0.110 0.258	0.288	-0.152 -0.046	-0.173	-0.111	0.169	
AA045192 R	Retinoblastoma 1 (including osteosarcoma) RETINOBLASTOMA BINDING PROTEIN 3	-0.135	0.383	0.163	0.086	0.324	0.547	
AA428365 R	RETINOBLASTOMA BINDING PROTEIN P48	-1.084 0.272	-0.395 0.318	-0.093 -0.160	-0.183 -0.204	-0.458 -0.119	0.610 0.275	
	Retinoblastoma-binding protein 1(alternative products) Retinoblastoma-like 1 (p107)	-0.036	0.127	0.116	-0.036	0.142	0.602	
N50554 R	RETINOBLASTOMA-LIKE PROTEIN 2	-0.499	-0.299	-0.481 -0.152	-0.577 -0.501	0.202 0.238	-0.270 0.111	
AA419238 R	RETINOIC ACID RECEPTOR BETA-2	0.209 1.335	0.145 0.458	-0.152 0.811	0.630	0.916	0.434	
AA633882 R	Retinoic acid receptor, gamma 1 Retinoi dehydrogenase 1 (11-cis)	0.401	0.695	0.437	0.545	0.270 0.476	0.573	
AA011014 R	Retinol-binding protein 3, interstitial	0.739 0.280	0.858 0.648	0.280 -0.373	0.385 0.052	-0.215	0.490	
N53959 R AA443302 R	Rhesus blood group, D antigen	-0.397	-0.037	0.240	0.179	0.005	0.634	
AA464544 R	RHOMBOTIN-2	-0.056 0.489	-0.032 -0.228	-0.931 -0.030	-1.370 0.252	-0.358 -0.376	-0.332 0.841	
T60163 R T70056 R	Ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent) Ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent) inhibitor	0.680	0.617	0.609	0.434	1.047	0.617	
AA485893 R	Ribonuclease, RNase A family, 1 (pancreatic)	0.451	0.285 -0.297	0.675 0.633	1.174 0.637	0.334 0.296	0.620	
R88243 R	Ribonuclease/angiogenin inhibitor RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1 CHAIN	0.268 1.073	-0.297 -0.086	1.686	0.507	0.829	0.450	
AA187351 R	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE MT CHAIN Ribonucleotide reductase M2 polypeptide	0.925	0.902	-0.082	-0.120	0.628	0.328 -0.500	
AA127100 R	Ribophorin I	0.214 0.450	-0.028 0.614	0.145 0.413	-0.013 0.201	0.436 0.531	0.308	
N20072 R	RIBOSE 5-PHOSPHATE ISOMERASE	*****						

ACC Gene Name	ZR75	YY3	YY1 .	468 -1.244	MPI -0.409	231 0.364	(log base 2 ratio
AA485911 Ribosomal protein L17 AA083485 Ribosomal protein L19	-0.962 -0.492	0.311 -0.441	-0.902 -0.316	-0.773	-0.359	0.545	
AA464743 Ribosomal protein L21	-0.222	-0.471 1.408	-0.183 0.746	-0.958 0.501	-0.132 1.269	0.699 0.456	
AA599178 Ribosomal protein L27a AA063631 Ribosomal protein L3	2.279 -1.352	-0.728	-0.820	-1.861	-1.341	-0.517	
W15277 Ribosomal protein L31	-0.300 -0.236	0.098 -0.0 9 8	0.207 0.062	-0.374 -0.005	0.044 -0.343	-0.405 0.331	
R43544 Ribosomal protein L32 AA873351 Ribosomal protein L35a	0.044	0.268	0.135	0.026	0.526	0.415	
AA683077 Ribosomal protein L37	0.304 1.351	1.372 1.692	0.203 -0.073	0.106 0.111	0.351 0.590	0.789	
AA669359 Ribosomal protein L44 AA496880 Ribosomal protein L5	0.153	0.722	0.283	0.914	1.531	-0.536	
AA629808 Ribosomal protein L6	0.290	0.419 0.253	-0.260 -0.336	0.037 -0.299	1.017 0.798	-0.315 1.151	
AA412470 Ribosomal protein L7 H23422 Ribosomal protein L7a	0.109 -0.711	-0.621	-0.223	-0.412	-0.283	0.479	
AA629641 Ribosomal protein S13	-0.316	0.263 0.330	-0.156 0.232	0.264 0.954	0.286 0.617	0.544 0.597	
AA668301 Ribosomal protein S16 AA281057 Ribosomal protein S17	-0.192 0.303	0.169	-0.343	-0.107	0.224	0.529	
R63811 Ribosomal protein S25	0.466	0.442 0.553	0.435 -0.636	0.478 -0.245	0.567 0.584	0.438 0.020	
AA856556 Ribosomal protein S28 AA411343 Ribosomal protein S29	-0.852 -0.076	0.555	0.349	0.256	0.759	-0.671	
AA888182 Ribosomal protein S4, X-linked	-2.291 -0.156	-0.855 0.122	-0.783 0.098	-1.866 -0.353	-0.561 0.294	-0.084 0.326	
T69488 Ribosomal protein S4, Y-linked AA456616 Ribosomal protein S5	-0.018	0.378	0.692	0.399	0.666	0.377	
AA425446 RIBOSOMAL PROTEIN S6 KINASE	-0.348	0.198 0.309	0.138 0.372	0.101 0.255	0.193 0.474	0.454 0.526	
AA452574 Ribosomal protein S6 kinase, 90kD, polypeptide 2 N53351 Ric (Drosophila)-like (expressed in neurons)	-0.039 -2.072	-1.142	-0.925	-1.459	-1.057	0.522	
T64905 Rieger syndrome (solurshin)	-0.570 0.771	0.026 0.718	0.112 1.717	-0.324 1.028	-0.148 1.345	-0.331 -0.025	
AA425772 Ring finger protein 1 H72918 RING3 PROTEIN	0.771 0.231	0.312	0.360	0.046	0.484	0.072	
N74956 RNA polymerase II polypeptide B (140 kD)	0.282	0.639	0.119 -0.092	0.384 -0.077	0.982 0.228	0.575 0.222	
AA430656 RNA polymerase II, polypeptide C (33kD) AA815407 RYANODINE RECEPTOR, SKELETAL MUSCLE	-0.460 -0.426	0.141 -0.269	-0.091	-0.420	-0.074	0.438	
T77811 RYK receptor-like tyrosine kinase	0.697	1.576	-0.051 -0.096	0.286 0.360	0.939 0.657	0.358 1.031	
AA444051 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) AA055242 S100 calcium-binding protein A3 (formerly S100E)	-0.041 -0.156	0.386	0.326	0.530	0.301	0.427	
AA086471 S100 calcium-binding protein A8 (calgranulin A)	-0.208	0.250	0.254 0.146	0.466 0.269	0.510 0.204	0.350 0.235	
AA424045 S-100 PROTEIN, BETA CHAIN	0.296 0.336	-0.105 0.163	0.146	0.142	0.216	-0.006	
R32848 S-100P PROTEIN AA485626 S-adenosylhomocysteine hydrolase	0.134	0.304	0.348 0.420	0.161 0.087	0.052 0.371	0.136 0.631	
R82300 S-adenosylmethionine decarboxylase 1 T59245 S-ADENOSYLMETHIONINE SYNTHETASE GAMMA FORM	0.021 -0.396	0.239 0.014	0.326	0.479	-0.302	0.090	
T59245 S-ADENOSYLMETHIONINE SYNTHE TASE GAMMA FORM AA234982 Sarcoglycan, delta (35kD dystrophin-associated glycoprotein)	-0.280	0.975	0.415	0.089 -0.923	0.210 -0.638	0.066 0.342	
R55993 SEC14 (S. cerevisiae)-like AA775616 Secreted phosphoprotein 1 (osteopontin, bone siatoprotein I)	-1.194 0.892	-0.468 0.730	-0.879 0.312	0.443	0.888	0.510	
H27864 SECRETOGRANIN II PRECURSOR	0.134	0.248	-0.366	-0.176	-0.122 0.280	0.509 0.849	
AA670429 Secretory granule, neuroendocrine protein 1 (7B2 protein)	-0.337 -0.169	-0.038 -0.002	0.046 -0.086	0.286 -0.243	0.194	-0.226	
H00662 Selectin L (lymphocyte adhesion molecule 1)	0.136	0.591	-0.264	-0.598	-0.339 0.443	-0.351 0.134	
R52639 SERINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC	0.490 -0.104	0.213 -0.009	0.698 -0.003	0.285 0.035	0.556	0.134	
AA845156 Serine protease inhibitor, Kazal type 1 AA451792 SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, BETA ISOFORM	1.270	-0.208	1.385	0.655	1.845	0.589	
AA283125 SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1	0.227 -0.083	-0.945 0.145	0.174 0.205	0.245 0.566	-1.470 0.280	0.694	
A4136882 SERINE/THREONINE-PROTEIN KINASE RECEPTOR R1 PRECURSOR H43049 SERINE/THREONINE-PROTEIN KINASE RECEPTOR R3 PRECURSOR	-0.005	0.089	0.042	-0.183	-0.248	-0.284	
N68565 SERUM ALBUMIN PRECURSOR	0.198 0.273	0.137 0.282	0.078 -0.026	-0.157 0.017	0.047 0.326	0.023 0.148	
H25546 SERUM AMYLOID A PROTEIN PRECURSOR H73234 SERUM PROTEIN MSE55	0.294	0.105	-0.265	-0.179	0.077	0.608	
AA630734 SERYL-TRNA SYNTHETASE	0.770 0.255	-0.234 0.398	0.400 0.463	-0.134 0.275	-0.022 0.367	0.725 0.821	
AA608548 SET PROTEIN T69271 Sex hormone-binding globulin	0.316	0.175	0.111	0.049	0.275	0.945 0.696	
AA427595 SHB adaptor protein (a Src homology 2 protein)	-0.278 0.185	0.120 0.543	0.106 0.218	0.063 0.153	0.180 0.167	0.507	
AA598652 Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) AA169183 Sialyltransferase 8 (alpha-N-acetylneuraminate: alpha-2,8-sialytransferase, GD3 synthase)	0.120	0.392	0.074	0.317	0.440 0.510	0.681 0.532	
AA411407 Signal recognition particle 19 kD protein	-0.202 0.270	0.601 0.164	-0.107 0.191	0.107 0.324	-0.088	0.032	
AA599078 Signal recognition particle 54 kD protein R43360 Signal recognition particle 9 kD protein	0.322	0.181	0.113	0.311	0.224 0.116	0.694 0.644	
AA598621 Signal recognition particle receptor ('docking protein') AA450360 Signal sequence receptor, alpha	1.210 1.104	0.541 0.670	0.443 0.517	0.697 0.563	0.314	-0.167	
AA488075 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	-0.049	-0.546	0.660	-0.051	1.500 -0.328	0.673 0.912	
AA399410 Signal transducer and activator of transcription 3 (acute-phase response factor)	-0.203 -0.184	0.110	-0.357 0.227	-0.435 0.646	-0.137	-0.328	
AA280647 Signal transducer and activator of transcription 5A	0.535	0.532	-0.001	-0.189 0.434	0.289 0.023	0.209 0.384	
R51607 Similar to PROTEIN TRANSLATION INITIATION FACTOR SUI1 HOMOLOG R51607 Similar to PROTEIN TRANSLATION INITIATION FACTOR SUI1 HOMOLOG	0.242 0.834	-0.003 0.553	0.103 0.386	0.139	0.491	0.358	
AA485203 Single-stranded DNA-binding protein	1.824	0.379 0.246	1.770 0.872	0.535 1.197	1.337 0.066	0.203 0.156	
N31587 SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1 N45131 Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)	-0.001 0.058	0.330	0.140	0.685	-0.525	-0.044	
H29485 Siggren syndrome antigen B (autoantigen La)	-0.138 0.278	0.623 0.375	-0.179 0.440	0.172 0.215	1.049 0.248	0.401 -0.222	
AA844447 SKI-RELATED ONCOGENE SNON H08564 SM22-ALPHA HOMOLOG	0.225	0.362	-0.020	0.246	0.232	0.074	
W69211 Small inducible cytokine A11 (eotaxin)	0.121	0.466 0.373	0.205 -0.052	0.634 0.112	-0.018 0.505	0.254 0.661	
AA425102 Small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je) AA677522 Small inducible cytokine A3 (homologous to mouse Mip-1a)	-0.171 1.084	1.716	1.016	0.813	0.992	0.642	
H62864 Small inducible cytokine A4 (homologous to mouse Mip-1b)	-0.049	0.632	0.148 0.322	0.142 -0.261	0.725 0.515	0.575 0.357	
AA486072 Small inducible cytokine A5 (RANTES) AA678021 Small nuclear ribonucleoprotein polypeptide E	0.427 0.121	0.214 0.610	0.163	0.890	0.933	0.665	
T54926 Small nuclear ribonucleoprotein polypeptide N	0.558	0.609	0.405 0.107	1.180 0.090	0.277 0.481	0.475 0.419	
AA599116 Small nuclear ribonucleoprotein polypeptides B and B1 H16255 SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1	0.466 0.129	0.409	0.261	0.268	1.012	0.807	
AA043335 Small nuclear RNA activating complex, polypeptide 3, 50kD	-0.019	0.649 1.567	0.158 0.155	0.273 0.317	0.695 1.150	0.189 -0.112	
AA447684 Small proline-rich protein 1B (comifin) AA490477 Smooth muscle myosin heavy chain isoform SMemb ihuman, umbilical cord, fetal aorta, mRNA Partia	0.031 at, 0.157	0.879	0.233	0.007	0.827	0.342	
AA498809 SNF2 (sucrose nonfermenting, yeast, homolog)-like 1	0.132	0.306	0.346 0.055	0.341 0.019	0.433 -0.228	0.871 0.664	
N49856 SODIUM-AND CHLORIDE-DEPENDENT BETAINE TRANSPORTER AA775899 Sodium/potassium ATPase, gamma subunit	-0.048 -0.417	-0.109	0.177	-0.375	-0.243	0.281	
AAARRA17 Sodium/potassium-transporting ATPase beta-3 subunit	0.411	-0.061 -0.315	-0.394 -0.273	-0.345 -0.566	-0.245 -0.418	0.356 1.555	
AA043133 Solute carrier family 16 (monocarboxylic acid transporters), member 1	-0.569 0.476	0.520	0.020	0.214	0.388	0.545	·
R00833 Solute carrier family 2 (facilitated glucose transporter), member 2	0.471 0.557	0.444 0.547	0.143 0.334	0.155 0.249	0.637 0.597	0.686 0.555	
H38650 Solute carrier family 2 (facilitated glucose transporter), member 5		-0.394	-0.516	-0.185	-0.426	1.455	
Tecros Colute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3)	0.304	0.438 0.073	0.155 0.029	0.451 0.497	0.331 0.064	0.711 0.459	
W45518 Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	-0.039 -0.349	-0.236	-0.066	-0.007	-0.312	0.740	
pecces 4 Solute corrier family 6 (neurotransmitter transporter, noradrenalin), member 2	-0.358 iv∈ 0.662	-0.013 0.431	0.016 0.431	0.277 0.279	0.016 1.042	0.549 0.701	
AA458982 Solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amilloride sensiti	0.002	0.401	0101	J.=.			

	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
ACC Gene Name AA455389 Solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amilloride sensitive	0.720	0.669	0.469	0.543	0.897	0.468	(log base 2 lane
AA431849 SON DNA binding protein	0.621	1.065 0.094	0.027 0.186	0.316 0.362	1.224 -0.084	0.490 0.607	
AA700604 Sorbitol dehydrogenase	-0.043 0.334	0.510	0.234	0.282	0.605	0.596	
H60859 Sorcin AA449430 Sorting nexin 1	0.049	0.330	0.217	0.146	0.276	0.886 0.882	
AA775423 SOX-3 PROTEIN	0.524 0.748	0.779 0.822	0.218 0.024	0.517 0.186	0.645 0.417	0.872	
T81103 Sp2 transcription factor W31688 Sp3 transcription factor	0.436	0.551	0.294	0.321	0.657	1.273	
H95960 SPARC/osteonectin	0.082	0.295 -0.076	0.359 0.234	0.412 0.626	0.167 -0.256	0.310 0.273	
AA022561 Special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) T60117 Spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	0.039 -0.020	0.622	-0.135	0.289	0.164	0.527	
T60117 Spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) AA011320 Spectrin, beta, erythrocytic (includes sperocytosis, clinical type I)	0.128	0.411	0.112	0.542	0.434	0.075	
AA018591 Spectrin, beta, non-erythrocytic 1	0.388 0.164	0.119 0.184	0.306 0.341	0.642 0.037	0.039 0.530	0.863 0.786	
AA400437 SPERM ANTIGEN HE2 PRECURSOR AA669545 Spermidine synthase	0.232	0.501	0.716	0.616	0.412	0.599	
AA011215 Spermidine/spermine N1-acetyltransferase	0.624	0.548	0.310	0.130 -0.478	0.605 -0.428	0.393 0.405	
R58991 Spermidine/spermine N1-acetyltransferase mRNA, complete cds R58991 Spermidine/spermine N1-acetyltransferase mRNA, complete cds	-0.182 -0.419	-0.232 -0.056	-0.538 -0.515	-0.581	-0.299	-0.606	
R58991 Spermidine/spermine N1-acetyltransterase mRNA, complete cos AA416890 Sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	1.900	0.920	0.808	0.812	0.561	-0.005	
N71628 Spi-B transcription factor (Spi-1/PU.1 related)	0.334 0.401	0.168 0.366	0.341 0.249	-0.304 -0.432	-0.109 0.454	0.330 -0.129	
R10604 Spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant) AA026557 Spleen focus forming virus (SFFV) proviral integration oncogene spi1	-0.015	0.348	-0.065	-0.002	0.322	0.018	
AA598572 Spleen tyrosine kinase	0.225	0.273	-0.003	0.493	0.349 -0.178	-0.037 0.163	
AA405748 SPLICING FACTOR U2AF 65 KD SUBUNIT	0.155 0.712	-0.180 0.812	-0.594 0.526	-0.215 0.058	0.876	0.171	
AA454585 Splicing factor, arginine/serine-rich 2 AA398883 SQUAMOUS CELL CARCINOMA ANTIGEN 1	1.678	1.504	0.202	1.420	0.498	0.509	
AA453420 SRY (sex determining region Y)-box 4	0.159	0.325	0.579 0.388	0.881 0.513	0.034 0.498	-0.327 0.546	
AA400464 SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	0.174 0.183	0.623 -0.089	0.348	0.015	0.420	0.618	
AA873060 STATHMIN AA098896 STEROID HORMONE RECEPTOR ERR1	-0.646	-0.252	-0.036	-0.339	-0.224	1.284	
AA679454 Steroidogenic acute regulatory protein	0.059 0.191	0.226 0.072	0.212 -0.050	0.043 -0.345	0.073 -0.591	0.587 -0.019	
AA664009 Sterol carrier protein 2 R07296 Sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase)	0.045	0.431	0.285	0.102	0.558	0.743	
R07296 Sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) H15155 STERYL-SULFATASE PRECURSOR	0.214	0.479	0.266	0.077	0.801	1.196	
T94169 STRESS-ACTIVATED PROTEIN KINASE JNK1	0.537 -0.333	0.461 0.556	0.146 -0.655	0.138 -1.032	0.144 -0.221	0.420 0.137	
AA157286 STRESS-ACTIVATED PROTEIN KINASE JNK2	0.364	-0.173	0.207	0.267	0.500	-1.048	
AA447115 Stromal cell-derived factor 1 W51794 Stromelysin	2.895	1.789	1.300	0.796	1.887	0.808	
T70043 SUCCINATE DEHYDROGENASE	-0.076 0.258	0.166 0.356	0.084 0.399	-0.425 0.408	-0.212 0.692	0.947 0.955	
AA463510 Succinate dehydrogenase 1, iron surphur (Ip) subunit	0.329	0.656	0.318	0.559	0.300	1.462	
N72215 Sulfated glycoprotein 1 AA725397 Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring	0.054	-0.284	0.103	0.212	0.286	0.693 0.195	
AA599127 Superoxide dismutase 1 (Cu/Zn)	-0.170 0.005	0.089 -0.454	0.157 0.276	0.178 0.062	0.027 -0.554	-0.063	
AA488084 Superoxide dismutase 2, mitochondrial AA454160 Superoxide dismutase 3, extracellular	1.246	0.980	1.142	-0.021	0.885	0.539	
AA126200 Suppression of tumorigenicity 2	0.214	0.117	0.226	0.294	0.260	0.814 0.971	
AA487571 Surfactant, pulmonary-associated protein C	1.113 -0.300	0.919 -0.281	0.259 -0.460	0.469 -0.883	0.522 -0.482	1.440	
AA699560 Surfeit 1 AA663884 SYNAPTOSOMAL ASSOCIATED PROTEIN 25	0.536	0.965	0.456	0.716	-0.010	1.127	
AA683073 SYNAPTOTAGMIN I	0.305	0.599	0.299	0.313	-0.228	0.946 0.614	
AA074511 Syndecan 1	-1.173 0.280	-1.034 0.479	-1.429 -0.039	-1.770 -0.075	-1.388 0.487	-0.479	
AA045058 Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) AA148737 Syndecan 4 (amphiglycan, ryudocan)	1.353	0.529	0.443	0.465	0.618	1.076	
AAA521AR Syntayin 5A	-0.007	-0.328	-0.482	-0.582 -0.401	-0.645 -0.305	0.969 1.260	
AA699926 Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)	-0.158 0.360	-0.107 0.685	-0.158 0.105	0.171	0.846	0.938	
AA455067 Synuclein, alpha (non A4 component of amyloid precursor) AA427491 T cell receptor alpha-chain	0.650	0.462	0.256	0.310	0.724	1.190	
N50880 T cell receptor gamma chain	0.359	0.132	-0.111 0.446	-0.196 -0.129	0.144 0.340	0.477 1.218	
AA400234 T3 receptor-associating cofactor-1 [hurnan, fetal liver, mRNA, 2930 nt] AA446659 Tachvkinin 2 (substance K, neurokinin A, neurokinin 2, neuromedin L, neurokinin alpha, neuropeptide ł	0.283 0.083	0.135 -0.095	-0.049	0.053	0.088	0.651	
N50549 TATA box binding protein	0.443	0.562	0.450	-0.304	-0.023	0.980	
T51236 T-cell acute lymphocytic leukemia 1 (NOTE: redefinition of symbol)	-0.615 -0.676	-0.662 -0.164	-0.909 -0.366	-1.209 0.089	-1.105 -0.434	0.812 0.679	
T-64192 T-cell receptor, beta cluster AA670107 T-cell receptor, delta	0.701	0.291	0.423	0.497	0.251	0.411	
AA055946 T-CELL SURFACE GLYCOPROTEIN CD3 DELTA CHAIN PRECURSOR	0.495	0.684	-0.074	-0.084	-0.281 0.779	0.046 0.740	
AA406028 T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR	0.277 0.410	0.615 0.030	0.485 0.264	0.333 -0.041	0.540	0.809	
AA293671 T-CELL SURFACE GLYCOPROTEIN CD8 BETA.3 CHAIN PRECURSOR R46821 T-COMPLEX PROTEIN 1, ALPHA SUBUNIT	0.489	0.090	0.332	0.213	0.766	0.725	
AA629692 T-COMPLEX PROTEIN 1, EPSILON SUBUNIT	0.425 2.047	0.650 0.773	0.122 2.452	0.386 0.258	0.181 1.647	0.122 -0.016	
AA779321 Tec protein tyrosine kinase	1.034	0.773	0.880	0.106	0.680	0.408	
AA629591 Testis enhanced gene transcript AA868278 Testis specific protein 1 (probe H4-1 p3-1)	0.440	0.264	0.124	-0.049	0.595	0.310	
AA608988 Testis specific protein, Y-linked	-0.037 0.229	-0.464 0.291	0.023 -0.194	-0.636 0.000	-0.528 0.520	0.723 0.927	
AA453467 Testis-specific lactate dehydrogenase (LDHC4, LDHX) mRNA W73889 Tetranectin (plasminogen-binding protein)	0.825	-0.024	-0.034	-0.740	0.514	0.454	
AA677257 Thiopurine S-methyltransferase	0.396	0.494	0.894	0.401	0.516	-0.245 -0.163	
AA431967 Thioredoxin	0.091 0.584	-0.036 0.473	-0.597 0.378	-0.585 0.562	0.261 0.629	0.533	
AA464849 Thioredoxin reductase AA461065 Thiosulfate sulfurtransferase (rhodanese)	-0.102	0.147	0.135	0.157	0.336	0.741	
AA630628 Threonyl-tRNA synthetase	-0.367	-0.715	-0.389	-0.747	-0.797 0.697	0.786 0.834	
H59861 Thrombomodulin	0.474 -0.126	0.478 0.064	0.273 -0.053	0.090 -0.518	-0.023	0.847	
AA479058 Thrombopoletin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and develo AA280514 Thrombopoletin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and develo	0.263	0.278	-0.156	0.455	0.031	0.436	
AA464532 Thrombospondin 1	0.176	0.300	0.105	-0.080	0.509 0.097	1.525 0.680	
H38240 Thrombospondin 2	0.005 -0.110	0.149 0.109	-0.038 0.259	-0.057 0.124	0.298	0.225	
AA423957 Thrombospondin 4 AA039932 Thromboxane A2 receptor	0.511	0.332	-0.029	0.621	0.112	0.586	
R76437 THROMBOXANE-A SYNTHASE	0.478	0.225	0.765	0.387 0.434	0.324 0.373	0.509 0.814	
AA496283 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR	0.787 0.600	0.574 0.357	0.372 0.160	0.223	0.432	1.639	
AA778098 Thymidine kinase 1, soluble AA663310 Thymidylate synthase	-0.074	0.082	0.334	0.021	0.067	0.970	
AA676998 Thymopoietin	-0.356	0.031	0.108 0.058	-0.277 -0.039	0.068 -0.121	0.740 1.748	
AA486085 THYMOSIN BETA-10 AA486207 Thyroid autoantigen 70kD (Ku antigen)	0.024 0.232	-0.114 0.205	0.215	0.628	-0.704	0.683	
AA454168 Thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene nomolog)	0.688	0.443	0.648	0.427	0.828	0.186	
AA069596 THYROLIBERIN PRECURSOR	0.666 0.142	0.090 0.229	0.767 -0.118	0.057 -0.128	0.060 0.144	-0.568 0.461	
T72171 Thyroxin-binding globulin N59426 TiA1 cytotoxic granule-associated RNA-binding protein-like 1	-0.365	0.229	0.289	0.799	0.266	0.476	
H50344 Tight junction protein 1 (zona occludens 1)	0.386	0.482	0.251	0.088	0.617	0.540	
AA399473 TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR	0.210 0.070	0.218 0.235	0.008 0.185	0.330 0.577	0.199 0.032	0.330 0.361	
T50282 TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR H80215 Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	0.531	0.695	0.145	-0.109	0.550	-0.152	
AA486280. Tissue inhibitor of metalloproteinase 2	0.763	0.414	0.487	0.336	0.222 0.577	-0.225 0.270	
AA000153 Tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	0.608 0.721	0.280 0.731	0.490 0.537	0.276 0.712	0.577	0.303	
R47893 TONSILLAR LYMPHOCYTE LD78 BETA PROTEIN PRECURSOR R22050 Topoisomerase (DNA) II beta (180kD)	0.833	0.556	-0.023	-0.091	0.816	0.676	

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ACC	Gene Name	ZR75	YY3 0.148	YY1 0.668	468 0.229	MPI 0.146	231 0.661	(log base 2 ra
	TRANSCOBALAMIN I PRECURSOR	0.380 0.472	0.344	-0.008	-0.185	0.923	1.015	
AA490459	Transcobalamin II Transcription elongation factor B (SIII), polypeptide 1-like	0.434	0.224	0.510	0.202	0.476	0.182	
AA130003	Transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A)	0.870	0.472	0.273	0.465	0.309	-0.273	
H28344	TRANSCRIPTION ELONGATION FACTOR S-II	0.734	0.732	1.072	0.351	0.799	0.088	
AA496576	Transcription factor 11 (basic leucine zipper type)	0.509	0.724 0.473	0.410 0.381	-0.235 0.385	0.220 0.251	-0.521 -0.513	
AA488366	Transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	0.544 0.941	0.673	0.095	0.333	0.906	0.177	
AA026644	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0.133	-0.074	0.262	0.098	-0.050	0.233	
AA449118	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like) Transcription factor 7 (T-cell specific)	0.419	0.740	-0.179	0.081	1.143	0.988	
N63770	Transcription factor AP-2 beta (activating enhancer-binding protein 2 beta)	-0.072	-0.131	0.081	-0.322	0.324	1.563	
AA284693	Transcription factor AP-4 (activating enhancer-binding protein 4)	0.208	-0.036	-0.219	0.154	-0.189	0.754	
AA629904	Transcription factor COUP 2 (a.k.a. ARP1)	0.295	0.879	0.341	-0.194	0.263 0.019	0.008	
AA443547	TRANSCRIPTION FACTOR P65	0.093	0.012	0.092	-0.103 0.003	0.162	0.009	
AA258001	TRANSCRIPTION FACTOR RELB	0.371 -0.168	0.220 0.186	0.129 -0.050	-0.178	0.296	0.760	
AA455964	TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT	0.158	0.417	0.191	0.333	0.585	1.190	
AA479196	TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT TRANSCRIPTION INITIATION FACTOR TFIID 250 KD SUBUNIT	0.630	0.848	0.154	0.520	0.208	0.483	
T60168	Transcription termination factor, RNA polymerase I	0.577	0.407	0.364	0.492	0.328	0.753	
AA039370	TRANSCRIPTIONAL ENHANCER FACTOR TEF-1	0.117	0.132	0.096	0.445	0.534	0.790	
AA291389	TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNTI	0.273	0.491	0.272	0.018	1.073	-0.049 1.000	
AA704492	Transducin-like enhancer of split 4, homolog of Drosophila E(\$p1)	-0.058 -0.542	-0.308 -0.350	-0.208 0.300	-0.382 0.077	-0.459 0.358	0.937	
AA873564	TRANSDUCIN-LIKE ENHANCER PROTEIN 2	0.076	0.750	-0.166	-0.029	0.342	1.017	
	Transferrin	0.539	0.215	0.325	0.347	0.264	0.272	
AA487593	Transferrin receptor (p90, CD71) TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521	0.413	0.219	0.319	0.830	-0.118	0.885	
AA48/42/	Transforming growth factor beta	0.244	0.130	-0.101	-0.253	0.006	1.015	
R36467	TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR	0.095	0.429	0.072	0.170	0.659	0.636	
AA233738	Transforming growth factor, beta 2	0.330	0.598	0.168	0.184	0.275 1.027	0.962 0.653	
AA040617	Transforming growth factor, beta 3	1.530 -0.323	0.517 0.124	1.355 0.349	0.803 -0.261	0.207	1.003	
AA487034	Transforming growth factor, beta receptor II (70-80kD)	0.407	0.746	0.122	-0.128	0.219	0.899	
H62473	Transforming growth factor, beta receptor III (betaglycan, 300kD))	-0.218	-0.031	-0.072	-0.382	-0.193	-0.137	
AA633901	Transforming growth factor, beta-induced, 68kD	0.187	0.337	0.116	-0.215	0.374	0.520	
N90882	TRANSFORMING PROTEIN RHOB Transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)	0.145	0.018	-0.189	-0.090	0.413	-0.422	
AA017132	Transient receptor potential channel 1	0.463	0.967	0.335	0.081	0.085	1.135	
	Transition protein 1 (TP1)	-0.321	-0.098	-0.166	0.342	0.213	-0.199 -0.140	
AA070358	Transketolase (Wernicke-Korsakoff syndrome)	0.686	0.959	0.329 0.281	0.325 0.426	0.462 0.235	0.257	
AA457050	Treacher Collins syndrome susceptibility protein	0.600 0.908	0.388 0.490	0.160	0.203	0.380	0.827	
	TRICHOHYALIN	-0.697	-0.275	-0.451	-1.010	-1.139	1.441	
	Triosephosphate isomerase 1	1.323		0.643	0.469	1.538	0.678	
R39682	Tripeptidyl peptidase II TrkB {alternatively spliced} [human, brain, mRNA, 1870 nt]	0.179		-0.199	-0.092	-0.125	1.151	
R60301	Tropomodulin	-0.005		0.060	0.065	-0.104	1.166	
W58092	Tropomyosin alpha chain (skeletal muscle)	0.233		0.344	0.010	0.304	0.914 0.558	
AA477400	Tropomyosin beta chain (skeletal muscle)	-0.583		-0.572	-0.679 -0.333	-0.409 0.164	0.401	
	Troponin I (skeletal fast)	-0.214 0.664	0.038 0.213	0.247 0.410	0.488	0.400	0.280	
AA182848	Troponin I, skeletal, slow	0.008		0.117	0.713	0.463	0.322	
AA449932	TROPONIN T, FAST SKELETAL MUSCLE ISOFORM BETA	1.198		0.569	0.537	1.183	0.360	
N70734	Troponin T1, skeletal, slow Troponin T2 (cardiac)	0.235		0.441	-0.004	0.208	0.463	
AA664040	TRYPTOPHANYL-TRNA SYNTHETASE	0.322		0.650	0.697	0.305	0.278	
H37774	Tuberin	0.612		0.512	-0.048	0.436 0.477	-0.448 0.104	
AA180742	TUBULIN ALPHA-4 CHAIN	-0.033 0.051		0.087 0.100	0.260 0.132	-0.051	0.130	
T77733	Tubulin, gamma polypeptide	-1.333		-1.073	-1.334	-1.234	0.067	
AA150416	Tumor necrosis factor receptor 2 (75kD) TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR	0.955		0.490	0.383	0.485	0.076	
W92764	Tumor protein p53 (Li-Fraumeni syndrome)	0.380		0.329	-0.122	0.361	-0.081	
R39356	TUMOR-ASSOCIATED ANTIGEN CO-029	0.119		0.235	-0.036	0.165	0.928	
AA487893	TUMOR-ASSOCIATED ANTIGEN L6	-0.122		-0.218	-0.205	-0.095 0.344	0.200 0.028	
H23460	TUP1-like enhancer of split gene 1	0.245 0.434		0.328 0.234	0.248 0.578	0.262	0.460	
H12312	TXK tyrosine kinase	0.088		0.277	0.209	0.507	0.386	
N67048	Type 3 iodothyronine deiodinase TYPE-1A ANGIOTENSIN II RECEPTOR	. 0.545		0.130	0.159	0.477	-0.032	
H66070 N31933	Tyrosinase (oculocutaneous albinism IA)	0.247	0.092	0.273	0.378	0.353	-0.507	
H62527	Tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, beta polypeptide	0.571		0.520	0.464	0.484	0.208	
N69107	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	0.666		0.514	0.364 0.171	0.015 0.685	0.238 0.411	
AA486473	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	0.628		-0.008 0.046	0.171	0.125	0.519	
AA447751	Tyrosine hydroxylase	-0.373 0.765		0.266	0.297	0.753	0.027	
	TYROSINÉ-PRÔTEIN KINASE CSK	1.387		1.148	0.757	1.859	0.706	
R78541 H84481	TYROSINE-PROTEIN KINASE ITK/TSK TYROSINE-PROTEIN KINASE RECEPTOR ECK PRECURSOR	0.561		-0.069	-0.101	0.917	0.341	
N90246	TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR	0.187		0.184	0.010	0.173	0.037	
AA432062	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR	-0.496		-0.137 1.108	-0.369 1.049	0.237 0.849	0.886 0.095	
H02848	TYROSINE-PROTEIN KINASE RECEPTOR TIE-2 PRECURSOR	0.764 0.279		-0.150	-0.009	0.226	0.529	
R70488	U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A	0.650		0.731	0.967	0.434	0.335	
R02346	U1 snRNP 70K protein U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	0.145	0.283	0.399	0.446	0.643	0.084	
R17676	LIBIOLINGI -CYTOCHROME C REDUCTASE COMPLEX 11 KD PROTEIN PRECURSOR	0.714		0.783	0.185	0.919	0.591	
AA564284	LIBIOLISMOL CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN	-0.038		0.077	-0.126	0.347 1.050	0.943 0.477	
T67270	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUBUNIT VI REQUIRING PROTEIN	-0.135		1.105 -0.402	0.031 -0.436	-0.722	0.856	
AA663058	Ubiquinol-extochrome c reductase core protein II	-1.045 -0.161		-0.402	-0.198	-0.328	0.125	
AA448184	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR	-0.624		-0.048	-0.549	-0.565	0.319	
AA625632	Ubiquitin A-52 residue ribosomal protein fusion product 1 Ubiquitin A-52 residue ribosomal protein fusion product 1	-0.980		0.022	-0.575	-0.058	0.360	
	Ubiquitin activating enzyme E1	0.691		0.624	0.236	0.715	0.408	
AA670438	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L1	0.403		0.366	0.072	0.370	0.902	
N27190	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3	-0.200		-0.125 0.230	-0.307 0.069	-0.245 0.541	0.477 -0.081	
AA465536	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T	0.456 -0.184		-0.245	-0.356	0.032	-0.038	
	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE TRE-2 Ubiquitin protein ligase E3A (human papilloma virus E6-associated protein)	0.26		-0.011	0.174	-0.886	0.461	
W90381 N23454	Ubiquitin protein ligase E3A (numan papilioma virus E0-associated protein) Ubiquitin-activating enzyme E1, like	1.31	0.210	1.025	0.998	1.282	1.023	
M23434 AAROO173	Ubiquitin-conjugating enzyme E1A (RAD6 homolog)	0.47		0.368	0.257	0.447	1.309	
AA598492	Ublauitin-conjugating enzyme E2B (RAD6 homolog)	-0.020		-0.291	-0.192	0.258 0.739	-0.466 0.275	
H20743	UBIQUITIN-CONJUGATING ENZYME E2-CDC34 COMPLEMENTING	0.21		0.221 0.915	-0.042 -0.098	0.739	0.275	
A 4 5 2 0 0 7 5	L Ubiquitin_conjugating enzyme F2H (homologous to yeast UBC8)	1.43 0.02		-0.083	-0.098	-0.310	0.796	
AA487197	Ubiquitin-conjugating enzyme E2I (homologous to yeast UBC9)	-0.09		0.081	0.080	0.251	1.015	
N49405 N64628	Ubiquitin-like protein UBIQUITIN-LIKE PROTEIN GDX	0.24	B 0.472	-0.002	0.013	0.500	0.895	
N64628 T50788	LIDP discurpossyltransferase precursor (UGT2B15)	0.13	4 0.144	0.651	0.592	0.157	0.568	
H68509	UDP-GLUCURONOSYLTRANSFERASE 2B10 PRECURSOR, MICROSOMAL	-0.13		-0.241	-0.535	-0.016	0.060	
N53031	UDP-GLUCURONOSYLTRANSFERASE 284 PRECURSOR, MICROSOMAL	0.15		0.409 0.583	0.174 0.328	0.225 1.018	0.307 0.910	
H61243	Uncoupling protein 2 (mitochondrial, proton carrier)	0.50 0.39		0.353	0.635	0.606	0.787	
R51835	unknown EST	0.39		0.693	-0.217	-0.500	0.441	
R60313	unknown EST unknown EST	1.88		0.604	0.761	1.337	-0.744	
R51835	gillionii 201							

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	A Section 2	ZR75	YY3	YY1	468	MPI	231	(log base 2 ratio
ACC R52541	Gene Name unknown EST	-0.396	0.413	-0.358	0.038	0.188	-0.178	(10)
R56088	unknown EST	0.176	0.341	0.082	0.268 0.343	0.460 0.323	0.139 0.831	
R60313	unknown EST	0.278 -1.505	0.101 -0.416	0.525 -0.890	-1.413	-0.715	1.015	
R36958 R51865	unknown EST unknown EST	0.278	0.091	0.243	0.160	0.087	0.272	
H07132	unknown EST	0.422	0.330	0.178	0.541	0.486	0.028	
N21573	unknown EST	-0.696 -0.335	-0.353 -0.280	-0.164 0.182	0.027 0.473	-0.311 -0.151	-0.229 0.873	
H08808 H05439	unknown EST unknown EST	-0.333	-0.014	0.285	0.617	0.038	0.699	
R51835	unknown EST	1.144	0.436	-0.170	0.250	-0.068	0.990	
R60313	unknown EST	-0.185	0.456	-0.376	-0.010	-0.460 1.697	0.723 -1.109	
R51835	unknown EST	1.498 0.584	1.963 0.416	0.782 0.377	0.701 0.034	-0.006	0.405	
R52541 R56088	unknown EST unknown EST	0.340	0.409	-0.148	-0.090	0.213	0.662	
R60313	unknown EST	0.489	0.608	0.019	0.188	0.538	0.452	
R36958	unknown EST	0.854 0.445	0.784 0.327	0.361 -0.064	0.164 -0.283	0.438 -0.107	0.541 0.827	
R51865	unknown EST unknown EST	0.239	0.530	0.161	0.076	0.325	0.499	
H07132 N21573	unknown EST	0.046	0.610	-0.132	-0.248	-0.170	-0.696	
H08808	unknown EST	0.909	0.690	0.057 -0.151	-0.334 -0.422	0.061 -0.294	0.319 0.844	
H05439	unknown EST	0.138 -0.509	0.655 -0.384	-0.186	-0.228	0.089	1.087	
H15112	Uracil-DNA glycosylase URACIL-DNA GLYCOSYLASE 1 PRECURSOR	0.085	0.217	-0.388	-0.164	-0.087	1.076	
AA426227	Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase	-0.120	0.005	-0.004	-0.348	0.086	0.112 0.135	
AA284669	Urokinase-type plasminogen activator	0.183 0.177	-0.027 0.000	0.108 0.212	-0.062 0.034	0.155 0.103	0.133	
AA424344 AA443089	Uroporphyrinogen decarboxylase Uroporphyrinogen III synthase	0.119	0.030	0.762	0.184	-0.085	0.042	
T63761	Uteroglobin	0.218	0.129	0.151	0.138	0.060	0.827	
AA676840	UTROPHIN	-0.176	-0.005 0.474	-0.071 1.329	0.023 0.561	-0.211 1.349	0.745 0.816	
	V-abi Abelson murine leukemia viral oncogene homolog 1	1.536 0.212	-0.031	0.433	0.520	0.026	0.058	
AA486080	Vacuolar H+ ATPase proton channel subunit V-akt murine thymoma viral oncogene homolog 1	-0.099	-0.171	-0.366	-0.115	-0.221	0.162	
AA457097	V-akt murine thymoma viral oncogene homolog 2	0.175	0.492	0.898	0.675	-0.089 0.337	1.460 0.809	
	VALYL-TRNA SYNTHETASE	1.455 0.387	0.892 0.202	0.251 0.538	0.480 0.501	0.602	0.003	
H16591	Vascular cell adhesion molecule 1 Vascular endothelial growth factor	0.436	0.554	0.256	0.502	-0.002	1.096	
R45059 AA630120	Vascular endothelial growth factor B	-0.078	-0.141	-0.470	-0.167	0.214	0.994	
H73241	VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR	0.083	0.400	-0.020 1.146	0.031 0.772	0.247 1.247	0.045 1.198	
	Vasodilator-stimulated phosphoprotein	0.707 -0.440	-0.159 -0.208	-0.452	0.128	0.494	0.569	
N24966	Vav 2 oncogene V-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3 (alternative products)	2.122	1.652	1.176	0.575	1.267	0.936	
H96235	V-ets avian erythroblastosis virus E26 oncogene homolog 2	0.088	0.289	0.706	0.546	0.171	1.036 1.285	
AA876039	VILLIN	-0.054 -0.310	0.201 0.005	0.097 0.492	-0.211 0.325	0.024 0.080	0.411	
AA411440 AA486321	Vilin 2 (ezrin)	0.712	0.439	0.809	0.695	1.179	0.833	
AA486728	Vinculin	0.242	0.049	0.066	0.056	0.023	0.978	
H65066	Visinin-like 1	0.225	0.402	0.357	0.420 0.075	0.057 0.303	1.214 1.022	
	Vitamin D (1,25- dihydroxyvitamin D3) receptor	0.350 0.519	-0.003 1.230	0.249 -0.225	-0.009	-0.040	1.251	
T68102	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE VITAMIN K-DEPENDENT PROTEIN Z PRECURSOR	0.482	0.499	-0.103	0.311	0.332	0.553	
AA461527	V-iun avian sarcoma virus 17 oncogene homolog	-0.154	-0.183	-0.066	-0.234	-0.043 0.412	0.677 0.976	
N24824	V-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	-0.420 -0.486	0.130 0.148	0.036 -0.929	-0.243 -0.698	-0.191	1.098	
AA457034	V-myb avian myeloblastosis viral oncogene homolog-like 2 V-myc avian myelocytomatosis viral oncogene homolog	-0.020	0.009	0.526	0.248	0.118	0.980	
AA044059	Voltage-dependent anion channel 1	-0.230	0.324	-0.213	0.078	0.552	1.052	
T66814	Voltage-dependent anion channel 2	-0.116 0.189	0.241 0.258	0.091 0.588	0.145 0.324	0.704 0.655	0.645 0.838	
R54176	Von Hippel-Lindau syndrome	0.169	0.260	0.438	0.049	0.001	0.841	
AA442994	VON WILLEBRAND FACTOR PRECURSOR V-raf murine sarcoma 3611 viral oncogene homolog 1	0.750	0.771	0.399	0.259	0.498	0.568	
W88566	V-raf murine sarcoma viral oncogene homolog B1	0.579	0.608	-0.039 -0.064	-0.279 -0.082	0.309 -0.095	0.907 0.794	
N25425	V-raf-1 murine leukemia viral oncogene homolog 1 V-raf simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	0.225 0.046	0.323 -0.159	-0.163	-0.163	0.185	0.788	
W15297 N32146	V-rel avian reticuloendotheliosis viral oncogene homolog	-0.321	0.079	-0.053	-0.306	-0.378	0.705	
W69471	V-ski avian sarcoma viral oncogene homolog	0.655	0.603	0.327 · 0.013	0.157 0.234	0.566 0.120	0.680 0.727	
T50498	V-ski avian sarcoma viral oncogene homolog	0.330 0.558	0.295 0.476	0.013	-0.708	0.120	0.510	
R83837	V-yes-1 Yamaguchi sarcoma viral related oncogene homolog s WEE1-LIKE PROTEIN KINASE	0.283	0.842	0.222	0.248	0.438	0.657	
AA131527	WHITE PROTEIN HOMOLOG	0.382	0.250	-0.106	-0.087	0.470	1.403 0.709	
	Wilms tumor 1	-0.088 0.481	0.427 0.488	0.063 -0.154	0.328 0.145	0.540 0.427	0.912	
N78828 W49672	Wingless-type MMTV integration site 2, human homolog Wingless-type MMTV integration site 5A, human homolog	-0.046	-0.006	0.248	0.252	0.172	0.907	
H61193	Wiskott-Aldrich syndrome (ecezema-thrombocytopenia)	0.350	0.446	0.531	0.396	0.432	1.010	
AA394240	X BOX BINDING PROTEIN-1	1.179 -1.296	1.208 -0.329	0.381 -0.411	0.798 -1.085	0.782 -0.828	0.618 0.390	
R09503	Xanthine dehydrogenase X-arrestin	0.516	0.891	0.006	0.668	0.558	0.874	
H86518 AA485380	X=arresuri XE169 PROTEIN	0.489	0.558	0.111	0.168	0.377	0.780	
AA453300	Xeroderma pigmentosum, complementation group A	0.206 0.587	0.093 0.534	0.143	0.017 0.059	0.123 0.403	0.194 1.180	
	5 X-LINKED HELICASE II	0.032	0.236	0.000	0.205	0.147	0.929	
H19440	7 YY1 transcription factor ZAKI-4 mRNA in human skin fibroblast, complete cds	0.127	0.344	-0.060	0.201	0.197	0.724	
AA877082	2 Zinc finger protein 10 (KOX 1)	0.309	0.511	-0.080	0.096	0.559 -0.649	0.729 0.610	
	Zinc finger protein 131 (clone pHZ-10)	-0.147 0.163	0.182 0.028	-0.447 0.270	-0.543 0.666	-0.009	0.998	
H17048 N67262	Zinc finger protein 133 (clone pHZ-13) Zinc finger protein 135 (clone pHZ-17)	-0.068	0.079	-0.109	0.098	0.040	0.742	
	3 Zinc finger protein 137 (clone pHZ-30)	-0.217	0.010	0.087	-0.133	0.221	0.664	
AA21150	3 Zinc finger protein 139 (clone pHZ-37)	-0.066 0.151	0.125 0.044	0.101 0.163	-0.188 -0.365	0.158 0.387	1.081 1.072	
AA443659 N26148	2 Zinc finger protein 143 (clone pHZ-1) Zinc finger protein 148 (pHZ-52)	0.010	-0.163	-0.616	-0.981	-0.609	-0.191	
AA43637	2 Zinc finger protein 151 (pHZ-67)	-0.035	0.114	0.268	0.247	-0.176	0.236	
AA70019	5 Zinc finger protein 174	0.450 -0.045	0.279 0.215	0.383 0.382	0.577 0.337	0.058 0.245	0.743 0.913	
T57877	Zinc finger protein 3 (A8-51) Zinc finger protein 35 (clone HF.10)	-0.045 0.417	0.215	0.382	0.337	0.245	0.466	
N64607 AA27994	2 Inc finger protein 35 (clone Hr.10) 1 Zinc finger protein 42 (myeloid-specific retinoic acid-responsive)	0.510	0.535	0.302	0.007	-0.001	0.606	
AA77389	4 Zinc finger protein 43 (HTF6)	0.936	0.762	0.819	0.152 -0.137	0.200 -0.128	-0.081 1.122	
AA62983	8 Zinc finger protein 74 (Cos52)	-0.196 0.582	0.009	-0.069 0.282	0.272	0.488	0.632	
AA62601 N69908	Zinc finger protein 76 Zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	0.620	0.663	0.034	-0.111	0.806	0.459	
R26526	Zinc finger protein basonuclin	-0.138	0.147	0.425	0.567	-0.170	0.686	
AA08843	4 ZINC FINGER PROTEIN HF.12	0.217 0.557	0.475 0.484	0.041 0.476	0.180 0.311	-0.047 0.135	0.172 1.273	
R38383 N77807	Zinc finger protein homologous to Zfp-36 in mouse ZINC FINGER PROTEIN HRX	0.809	0.920	0.983	1.969	0.247	1.194	
	2 Zinc Finger protein, X-linked	0.264	0.260	0.162	0.433	-0.197	0.742	
AA86246	5. Zinc-alpha-2-plycoprotein 1	0.566 -0.251	0.355 -0.258	-0.308 1.777	0.286 0.198	0.338 1.423	-0.032 1.369	
AA42560	2 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR	-0.201	-0.200		0.,00			

Personnel Supported by this Award

Brent H. Cochran, Ph.D. Nicholas Grammatikakis, Ph.D.

Publications resulting from this award:

- 1 .Grammatikakis, N., Lin, J.-H., Grammatikakis, A., Tsichlis, P. N. and Cochran, B. H. (1999). p50^{cdc37} acting in concert with Hsp90 is required for Raf-1 function. Mol. Cell Biol. *19*, 1661-1672.
- 2. Silverstein, A. M., Grammatikakis, N., Cochran, B. H., Chinkers, M. and Pratt, W. B. (1998). p50(cdc37) binds directly to the catalytic domain of Raf as well as to a site on hsp90 that is topologically adjacent to the tetratricopeptide repeat binding site. J Biol Chem 273, 20090-5.